

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 35.1493 Seconds
(without alignments)
120.578 Million cell updates/sec

Title: US-09-641-802-5
Perfect score: 81
Sequence: 1 DLEMPVLPVEPFPPFV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8						
Result		Query						
No.	Score	Match	Length	DB	ID		Description	
1	81	100.0	15	4	AAB72504	Aab72504	Colostrin	
2	81	100.0	15	4	AAB59322	Aab59322	Ewe colos	
3	81	100.0	15	4	AAB72250	Aab72250	Colostrin	
4	81	100.0	15	4	AAB72536	Aab72536	Colostrin	
5	81	100.0	15	5	AAO14581	Aao14581	Neural ce	
6	81	100.0	15	5	AAM51040	Aam51040	Colostrin	
7	81	100.0	15	5	AAE20232	Aae20232	Colostrin	
8	81	100.0	16	4	AAB59352	Aab59352	Ewe colos	
9	57	70.4	10	4	AAE07187	Aae07187	Colostrin	

10	51	63.0	10	4	AAE07197	Aae07197 Modified
11	39.5	48.8	15	5	AAU77172	Aau77172 Transcrip
12	36	44.4	18	4	AAB72520	Aab72520 Colostrin
13	36	44.4	18	4	AAB59330	Aab59330 Ewe colos
14	36	44.4	18	4	AAB72267	Aab72267 Colostrin
15	36	44.4	18	4	AAB72552	Aab72552 Colostrin
16	36	44.4	18	5	AAO14598	Aao14598 Neural ce
17	36	44.4	18	5	AAM51056	Aam51056 Colostrin
18	36	44.4	18	5	AAE20249	Aae20249 Colostrin
19	34	42.0	14	2	AAR93469	Aar93469 GST-SRC p
20	34	42.0	15	4	AAB72507	Aab72507 Colostrin
21	34	42.0	15	4	AAB59313	Aab59313 Ewe colos
22	34	42.0	15	4	AAB72253	Aab72253 Colostrin
23	34	42.0	15	4	AAB72539	Aab72539 Colostrin
24	34	42.0	15	5	AAO14584	Aao14584 Neural ce
25	34	42.0	15	5	AAM51043	Aam51043 Colostrin
26	34	42.0	15	5	AAE20235	Aae20235 Colostrin
27	34	42.0	15	5	ABB09569	Abb09569 Human Ll
28	34	42.0	16	4	AAB59344	Aab59344 Ewe colos
29	34	42.0	18	6	AAE34144	Aae34144 T-cell st
30	33	40.7	14	2	AAR58339	Aar58339 Hypotensi
31	32	39.5	15	2	AAW85209	Aaw85209 Helper T-
32	32	39.5	15	2	AAW85195	Aaw85195 Helper T-
33	32	39.5	15	2	AAW85329	Aaw85329 Helper T-
34	32	39.5	15	4	ABP24661	Abp24661 HIV DR su
35	32	39.5	15	4	ABP24658	Abp24658 HIV DR su
36	32	39.5	16	2	AAR29099	Aar29099 Chymotryp
37	31.5	38.9	18	6	ADB12816	Adb12816 Antihyper
38	31	38.3	10	2	AAR93548	Aar93548 Random 10
39	31	38.3	10	4	AAB75678	Aab75678 HLA class
40	31	38.3	10	6	ABR47334	Abr47334 Staphyloc
41	31	38.3	10	6	ABR47208	Abr47208 Staphyloc
42	31	38.3	12	6	ABR75157	Abr75157 Elemental
43	31	38.3	12	7	ADB67069	Adb67069 GaAs bind
44	31	38.3	13	3	AAY57715	Aay57715 Human clu
45	31	38.3	18	3	AAY57716	Aay57716 Human clu
46	30	37.0	9	6	ABR25398	Abr25398 Human can
47	30	37.0	9	6	ABR24394	Abr24394 Human can
48	30	37.0	9	6	ABR24628	Abr24628 Human can
49	30	37.0	9	6	ABR25632	Abr25632 Human can
50	30	37.0	9	6	ABR24838	Abr24838 Human can
51	30	37.0	9	6	ABR25012	Abr25012 Human can
52	30	37.0	10	6	ABR24490	Abr24490 Human can
53	30	37.0	10	6	ABR24879	Abr24879 Human can
54	30	37.0	10	6	ABR25765	Abr25765 Human can
55	30	37.0	10	6	ABR25070	Abr25070 Human can
56	30	37.0	10	6	ABR24761	Abr24761 Human can
57	30	37.0	11	7	ADE15739	Ade15739 E. coli t
58	30	37.0	12	7	ADE15738	Ade15738 E. coli t
59	30	37.0	13	4	AA71992	Aay71992 Autotaxin
60	30	37.0	13	7	ADE15737	Ade15737 E. coli t
61	30	37.0	14	7	ADE15736	Ade15736 E. coli t
62	30	37.0	15	2	AAR79631	Aar79631 Endocardi
63	30	37.0	15	2	AAW23515	Aaw23515 Purified
64	30	37.0	15	2	AAW57794	Aaw57794 Fatty aci
65	30	37.0	15	3	AA797960	Aay97960 Phage lib
66	30	37.0	15	6	ABR38016	Abr38016 Human can

67	30	37.0	15	6	ABR37873	Abr37873	Human can
68	30	37.0	15	6	ABR37911	Abr37911	Human can
69	30	37.0	15	6	ABR37915	Abr37915	Human can
70	30	37.0	15	6	ABR37944	Abr37944	Human can
71	30	37.0	15	6	ABR37800	Abr37800	Human can
72	30	37.0	15	6	ABR37857	Abr37857	Human can
73	30	37.0	15	6	ABR37890	Abr37890	Human can
74	30	37.0	15	7	ADE15735	Adel15735	E. coli t
75	30	37.0	16	2	AAW39049	Aaw39049	Peptide r
76	30	37.0	16	7	ADE15734	Adel15734	E. coli t
77	30	37.0	17	2	AAR58340	Aar58340	Hypotensi
78	30	37.0	17	2	AAW39044	Aaw39044	Peptide r
79	30	37.0	17	6	ABP55570	Abp55570	DPP10 C-t
80	30	37.0	17	7	ADC22248	Adc22248	Protein b
81	30	37.0	17	7	ADE15733	Adel15733	E. coli t
82	30	37.0	18	6	ABP82709	Abp82709	G protein
83	30	37.0	18	7	ADE15732	Adel15732	E. coli t
84	29	35.8	9	5	ABB97104	Abb97104	Human tum
85	29	35.8	10	6	ABR47319	Abr47319	Staphyloc
86	29	35.8	10	7	ADE15740	Adel15740	E. coli t
87	29	35.8	11	2	AAW03290	Aaw03290	CNS-inhib
88	29	35.8	13	2	AAR83665	Aar83665	Insect ha
89	29	35.8	13	2	AAW03291	Aaw03291	CNS-inhib
90	29	35.8	14	2	AAW38060	Aaw38060	PPPPY mot
91	29	35.8	14	7	ADB49250	Adb49250	Biotinylna
92	29	35.8	15	2	AAR79630	Aar79630	Endocardi
93	29	35.8	15	6	ABP59108	Abp59108	Flavoprot
94	29	35.8	15	6	ABR31644	Abr31644	Human can
95	29	35.8	15	6	ABR32150	Abr32150	Human can
96	29	35.8	15	6	ABR31883	Abr31883	Human can
97	29	35.8	16	2	AAW39007	Aaw39007	Peptide r
98	29	35.8	16	2	AAW25416	Aaw25416	Crk N-ter
99	29	35.8	17	2	AAY22119	Aay22119	Human uri
100	29	35.8	17	3	AAB34947	Aab34947	Gene 22 h

ALIGNMENTS

RESULT 1

AAB72504

ID AAB72504 standard; peptide; 15 AA.

XX

AC AAB72504;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #5.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.
 XX
 PR 17-AUG-1999; 99US-0149310P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the cell
 PT with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations.
 XX
 PS Claim 6; Page 25; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPFPPFV 15
 |||||
 Db 1 DLEMPVLPVEPFPPFV 15

RESULT 2

AAB59322

ID AAB59322 standard; peptide; 15 AA.

XX

AC AAB59322;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment B-7.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.
XX
PS Claim 7; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPFPPFV 15
| | | | | | | | | | | | | | |
Db 1 DLEMPVLPVEPFPPFV 15

RESULT 3

AAB72250

ID AAB72250 standard; peptide; 15 AA.

XX

AC AAB72250;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 5.

XX

KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological diosrder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

XX

OS Synthetic.

XX

PN WO200111937-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022818.

XX

PR 17-AUG-1999; 99US-0149311P.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX

DR WPI; 2001-202804/20.

XX

PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator.

XX

PS Claim 1; Page 34; 50pp; English.

XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokines. Colostrinin and its derived peptides are useful for inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPFPPFV 15

|||||||

Db 1 DLEMPVLPVEPFPPFV 15

RESULT 4

AAB72536

ID AAB72536 standard; peptide; 15 AA.

XX

AC AAB72536;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #5.

XX

KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.

XX

PD 22-FEB-2001.

XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX
 PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPFPPFV 15
 |||||
 Db 1 DLEMPVLPVEPFPPFV 15

RESULT 5

AAO14581

ID AAO14581 standard; peptide; 15 AA.

XX

AC AAO14581;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 5.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022777.

XX

PR 17-AUG-2000; 2000WO-US022777.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Boldogh I, Stanton JG, Hughes TK;

XX

DR WPI; 2002-269152/31.

XX

PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog.

XX

PS Claim 7; Page 21; 37pp; English.

XX

CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 5; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPFPPFV 15

|||||||

Db 1 DLEMPVLPVEPFPPFV 15

RESULT 6

AAM51040

ID AAM51040 standard; peptide; 15 AA.

XX

AC AAM51040;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide.

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "optional C-terminal amidation"

XX

PN WO200213849-A1.

XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022775.
XX
PR 17-AUG-2000; 2000WO-US022775.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2002-269150/31.
XX
PT Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 1; Page 34; 54pp; English.
XX
CC The present sequence is that of a colostrinin constituent peptide that is
CC preferred for use as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified as having
CC a beta-casein homologue precursor. Methods are claimed for: inducing a
CC cytokine in a cell by contact with an immunological regulator, where the
CC cell is present in a cell culture, a tissue, an organ or an organism, and
CC the cell is mammalian, including human; modulating an immune response in
CC a cell by contact with the immunological regulator under conditions
CC effective to induce a cytokine; modulating an immune response in a
CC patient by administering an immunological regulator under conditions
CC effective to induce a cytokine, where the immunological regulator is
CC administered topically or as part of a dietary supplement, and where the
CC immune response is specific or non specific, an interferon response or an
CC antibody response; modulating blood cell proliferation by contacting
CC blood cells with a blood cell regulator, where the blood cells are
CC present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patent. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha, interleukin-6 and interleukin-10
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPFPPV 15
| | | | | | | | | | | | | | |
Db 1 DLEMPVLPVEPFPPV 15

RESULT 7
AAE20232
ID AAE20232 standard; peptide; 15 AA.

XX
 AC AAE20232;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostrinin constituent peptide #5.
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnerary.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "Optionally C-terminal amide"
 XX
 PN WO200213850-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022776.
 XX
 PR 17-AUG-2000; 2000WO-US022776.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2002-269151/31.
 XX
 PT Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog.
 XX
 PS Claim 6; Page 25; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress level
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
 CC organ, or organism; or for treating oxidative damage to the skin of a
 CC patient e.g. animal or human; to modulate oxidative stress during/ after
 CC a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPFPFV 15
| | | | | | | | | | | | | | |
Db 1 DLEMPVLPVEPFPFV 15

RESULT 8

AAB59352

ID AAB59352 standard; peptide; 16 AA.

XX

AC AAB59352;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #12.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 81; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPFPPFV 15
| | | | | | | | | | | | | | |
Db 2 DLEMPVLPVEPFPPFV 16

RESULT 9

AAE07187

ID AAE07187 standard; peptide; 10 AA.

XX

AC AAE07187;

XX

DT 06-NOV-2001 (first entry)

XX

DE Colostrinin peptide 3.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;

KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;

KW central nervous system disorder; neurodegenerative disorder; weight loss;

KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;

KW acquired immunological deficiency; neurological disorder; dementia;

KW antiviral.

XX

OS Unidentified.

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-488775/53.

XX

PT Peptide useful as an interalia in the treatment of e.g. disorders of the

PT immune system and the central nervous system comprises ten amino-terminal

PT amino acid sequence derived from peptides present in colostrinin.

XX

PS Claim 1; Page 15; 40pp; English.

XX

CC The invention relates to colostrinin peptide fragments which are useful,

CC inter alia, in the treatment of chronic disorders of the immune system

CC and the central nervous system. Colostrinin peptides are used as a

CC medicament in the treatment of neurological disorders e.g., dementia,

CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron

CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and

CC neurosis, in acquired immunological deficiencies, chronic bacterial and

CC viral infections and diseases characterised by the presence of beta-

CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxillary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is colostrinin peptide 3 related to the invention
 XX
 SQ Sequence 10 AA;

Query Match 70.4%; Score 57; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLPEPFPPF 14
 |||||
 Db 1 PVLPEPFPPF 10

RESULT 10

AAE07197

ID AAE07197 standard; peptide; 10 AA.

XX

AC AAE07197;

XX

DT 06-NOV-2001 (first entry)

XX

DE Modified colostrinin cyclic peptide #3.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic
 FT linkage with Pro found at the C-terminal end"

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;
 XX
 DR WPI; 2001-488775/53.
 XX
 PT Peptide useful as an inter alia in the treatment of e.g. disorders of the
 PT immune system and the central nervous system comprises ten amino-terminal
 PT amino acid sequence derived from peptides present in colostrinin.
 XX
 PS Example 2; Page 8; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxillary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is modified colostrinin cyclic peptide #3 related to the
 CC invention
 XX
 SQ Sequence 10 AA;

Query Match 63.0%; Score 51; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLPVEFPF 13
 |||||
 Db 2 PVLPVEFPF 10

RESULT 11

AAU77172

ID AAU77172 standard; peptide; 15 AA.

XX

AC AAU77172;

XX

DT 02-JUL-2002 (first entry)

XX

DE Transcriptional control factor ZFM1 isomer 25.63 N-terminal peptide.

XX

KW Human; transcriptional control factor ZFM1 isomer 25.63; HIV;

KW malignant tumour; haemopathy; human immunodeficiency virus; cancer;

KW immunological disease; inflammation; cytostatic; haemostatic; virucide;

KW immunomodulatory; antiinflammatory; gene therapy.

XX

OS Homo sapiens.
 XX
 PN WO200220588-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 02-JUL-2001; 2001WO-CN001127.
 XX
 PR 07-JUL-2000; 2000CN-00117050.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-339796/37.
 XX
 PT Human transcriptional control factor ZFM1 isomer 25.63 and encoding
 PT polynucleotide, used in diagnosis and treatment of malignant tumors,
 PT hemopathy, human immunodeficiency virus infection, immunological diseases
 PT and inflammation.
 XX
 PS Example 5; Page 14; 38pp; Chinese.
 XX
 CC The invention relates to the human transcriptional control factor ZFM1
 CC isomer 25.63 and the polynucleotide encoding it. The sequences of the
 CC invention are used in diagnosis and treatment of malignant tumours,
 CC haemopathy, human immunodeficiency virus (HIV) infection, immunological
 CC diseases and various inflammations. This sequence represents the human
 CC transcriptional control factor ZFM1 isomer 25.63 N-terminal peptide, used
 CC in ELISA
 XX
 SQ Sequence 15 AA;

Query Match 48.8%; Score 39.5; DB 5; Length 15;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 4 MPVLPVEPFPPFV 15
 ||:| || ||||
 Db 1 MPIL-VEKFPPFV 11

RESULT 12

AAB72520

ID AAB72520 standard; peptide; 18 AA.

XX

AC AAB72520;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #21.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022665.
 XX
 PR 17-AUG-1999; 99US-0149310P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the cell
 PT with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations.
 XX
 PS Claim 6; Page 26; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient
 XX
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 4; Length 18;
 Best Local Similarity 50.0%; Pred. No. 92;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
 :: | ||||
 Db 3 EMPFPKYPVEPF 14

RESULT 13

AAB59330

ID AAB59330 standard; peptide; 18 AA.

XX

AC AAB59330;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment C-5.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;

KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX

PS Claim 7; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 4; Length 18;

Best Local Similarity 50.0%; Pred. No. 92;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12

:: | ||||

Db 3 EMPFPKYPVEPF 14

RESULT 14

AAB72267

ID AAB72267 standard; peptide; 18 AA.

XX

AC AAB72267;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 22.

XX

KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

XX

OS Synthetic.

XX

PN WO200111937-A2.

XX

PD 22-FEB-2001.

XX
 PF 17-AUG-2000; 2000WO-US022818.
 XX
 PR 17-AUG-1999; 99US-0149311P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator.
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrinin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 XX
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 4; Length 18;
 Best Local Similarity 50.0%; Pred. No. 92;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
 :: | ||||
 Db 3 EMPFPKYPVEPF 14

RESULT 15

AAB72552

ID AAB72552 standard; peptide; 18 AA.

XX

AC AAB72552;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #21.

XX

KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX
 PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 4; Length 18;
 Best Local Similarity 50.0%; Pred. No. 92;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLEMPVLPVEPF 12
 :: | ||||
 Db 3 EMPFPKYPVEPF 14

RESULT 16

AAO14598

ID AAO14598 standard; peptide; 18 AA.

XX

AC AAO14598;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 21.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022777.
 XX
 PR 17-AUG-2000; 2000WO-US022777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;
 XX
 DR WPI; 2002-269152/31.
 XX
 PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention
 XX
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 5; Length 18;
 Best Local Similarity 50.0%; Pred. No. 92;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
 :: | ||||
 Db 3 EMPFPKYPVEPF 14

RESULT 17

AAM51056

ID AAM51056 standard; peptide; 18 AA.

XX

AC AAM51056;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide (casein amino acids 121-138).

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "optional C-terminal amidation"
 XX
 PN WO200213849-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022775.
 XX
 PR 17-AUG-2000; 2000WO-US022775.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2002-269150/31.
 XX
 PT Modulation of blood cell proliferation in a patient involves use of blood
 PT cell regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide that is
 CC preferred for use as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. It is classified as having
 CC a beta-casein homologue precursor, and corresponds to casein amino acids
 CC 121-138. Methods are claimed for: inducing a cytokine in a cell by
 CC contact with an immunological regulator, where the cell is present in a
 CC cell culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell by
 CC contact with the immunological regulator under conditions effective to
 CC induce a cytokine; modulating an immune response in a patient by
 CC administering an immunological regulator under conditions effective to
 CC induce a cytokine, where the immunological regulator is administered
 CC topically or as part of a dietary supplement, and where the immune
 CC response is specific or non specific, an interferon response or an
 CC antibody response; modulating blood cell proliferation by contacting
 CC blood cells with a blood cell regulator, where the blood cells are
 CC present in a cell culture or an organism, are mammalian or human, and
 CC where the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A claimed
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an
 CC active agent such as the present peptide. Cytokines induced by this
 CC peptide in human leucocyte cultures include interferon-gamma, tumour
 CC necrosis factor-alpha and interleukin-10
 XX
 SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 5; Length 18;
 Best Local Similarity 50.0%; Pred. No. 92;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
 :: | ||||
 Db 3 EMPFPKYPVEPF 14

RESULT 18

AAE20249

ID AAE20249 standard; peptide; 18 AA.

XX

AC AAE20249;

XX

DT 18-JUN-2002 (first entry)

XX

DE Colostrinin constituent peptide #21.

XX

KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnerary.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "Optionally C-terminal amide"

XX

PN WO200213850-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022776.

XX

PR 17-AUG-2000; 2000WO-US022776.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Stanton GJ, Hughes TK, Boldogh I;

XX

DR WPI; 2002-269151/31.

XX

PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog.

XX

PS Claim 6; Page 26; 5lpp; English.

XX

CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient e.g. animal or human; to modulate oxidative stress during/ after
CC a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and

CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide
XX
SQ Sequence 18 AA;

Query Match 44.4%; Score 36; DB 5; Length 18;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
:: | ||||
Db 3 EMPFPKYPVEPF 14

RESULT 19

AAR93469

ID AAR93469 standard; peptide; 14 AA.

XX

AC AAR93469;

XX

DT 09-MAY-1996 (first entry)

XX

DE GST-SRC protein tyrosine kinase derived peptide #3.

XX

KW SH3 ligand; SH3 binding agent; biased phage library;

KW recognition sequence; src SH3 domain; Paget's disease; restenosis;

KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;

KW p67; complex; chronic myelogenous leukaemia; cancer.

XX

OS Synthetic.

XX

PN WO9524419-A1.

XX

PD 14-SEP-1995.

XX

PF 13-MAR-1995; 95WO-US003208.

XX

PR 11-MAR-1994; 94US-00209835.

PR 06-JAN-1995; 95US-00369832.

XX

PA (ARIA-) ARIAD PHARM INC.

XX

PI Rickles RJ, Brugge JS, Botfield MC, Zoller MJ;

XX

DR WPI; 1995-328231/42.

XX

PT Identification of peptide(s) binding specifically to SH3 domains - for

PT use in inhibiting interactions mediated by SH3 domains in treatment of

PT e.g. osteoporosis and cancer.

XX

PS Disclosure; Fig 5; 74pp; English.

XX

CC The sequences given in AAR93457-71 represent peptides which are SH3

CC ligands/SH3 binding agents. They represent a biased phage library which

CC comprises five random amino acids flanking the decapeptide -RSLRPLPPLP or

CC derivatives of this, which was identified as a recognition sequence for

CC the src SH3 domain. These sequences were identified using the method of
CC the invention. The method comprises contacting the SH3 domain with a
CC mixture of peptides under conditions permitting a ligand to bind to an
CC SH3 domain to form a complex. Any unbound peptides are removed and the
CC complexed peptide ligands are dissociated from the complexes. The
CC selected peptides are enriched by re-contacting them with the SH3 domain
CC and then candidates which bind to the SH3 domain are detected. The
CC isolated SH3 binding peptides may be used in the diagnosis, prevention
CC and treatment of conditions or diseases resulting from cellular processes
CC mediated by an SH3-based interaction. Such diseases include Paget's
CC disease. Other conditons treatable with these peptides include
CC restenosis, rheumatoid arthritis, gout and other problems in which an SH3
CC of neutrophil oxidase p47 and p67 complex is implicated, etc

XX

SQ Sequence 14 AA;

Query Match 42.0%; Score 34; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEFPF 13

| :| || | |

Db 3 LPLPPLPARPHP 14

RESULT 20

AAB72507

ID AAB72507 standard; peptide; 15 AA.

XX

AC AAB72507;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #8.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.

XX

PR 17-AUG-1999; 99US-0149310P.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Stanton GJ, Hughes TK, Boldogh I;

XX

DR WPI; 2001-218342/22.

XX

PT Modulating oxidative stress level in a cell, involves contacting the cell
PT with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations.

XX

PS Claim 6; Page 25; 48pp; English.

XX

CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient

XX

SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 4; Length 15;

Best Local Similarity 70.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEVPFPF 14

| | || ||

Db 5 PKLKVEVPFPF 14

RESULT 21

AAB59313

ID AAB59313 standard; peptide; 15 AA.

XX

AC AAB59313;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment A-4.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections; and diseases characterized
PT by amyloid plaques.

XX

PS Claim 7; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 4; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEVEFPF 14

| | | | |

Db 5 PKLKVEVFPF 14

RESULT 22

AAB72253

ID AAB72253 standard; peptide; 15 AA.

XX

AC AAB72253;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 8.

XX

KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

XX

OS Synthetic.

XX

PN WO200111937-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022818.

XX

PR 17-AUG-1999; 99US-0149311P.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX

DR WPI; 2001-202804/20.

XX

PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator.

XX

PS Claim 1; Page 34; 50pp; English.

XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokines. Colostrinin and its derived peptides are useful for inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies

XX

SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 4; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVL PVE PFPF 14

| | | | |

Db 5 PKL KVE VFPF 14

RESULT 23

AAB72539

ID AAB72539 standard; peptide; 15 AA.

XX

AC AAB72539;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #8.

XX

KW Neuroprotective; neural cell differentiation regulator; colostrinin;

KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022774.

XX

PR 17-AUG-1999; 99US-0149633P.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Boldogh I;

XX

DR WPI; 2001-226545/23.

XX

PT Use of colostrinin, its constituent peptide or analog as a neural cell

PT regulator, for promoting neural cell differentiation and treating damaged

PT neural cells in a patient.

XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 4; Length 15;
 Best Local Similarity 70.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEVPFPF 14
 | | | | |
 Db 5 PKLKVEVPFPF 14

RESULT 24

AAO14584

ID AAO14584 standard; peptide; 15 AA.

XX

AC AAO14584;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 8.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022777.

XX

PR 17-AUG-2000; 2000WO-US022777.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Boldogh I, Stanton JG, Hughes TK;

XX

DR WPI; 2002-269152/31.

XX

PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog.

XX

PS Claim 7; Page 21; 37pp; English.

XX

CC The invention comprises a method for promoting cell differentiation (e.g. neural cell differentiation). The method involves contacting cells with a neural cell regulator (i.e. a colostrinin peptide) in order to change the cells in morphology to form neural cells. Colostrinin is a proline-rich polypeptide aggregate that is present in colostrum. The method of the invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention

XX

SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 5; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEVPFPF 14
| | | | |
Db 5 PKLKVEVPFPF 14

RESULT 25

AAM51043

ID AAM51043 standard; peptide; 15 AA.

XX

AC AAM51043;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide.

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "optional C-terminal amidation"

XX

PN WO200213849-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022775.

XX

PR 17-AUG-2000; 2000WO-US022775.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX

DR WPI; 2002-269150/31.

XX

PT Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrinin, its constituent peptide and/or
PT analog.

XX

PS Claim 1; Page 34; 54pp; English.

XX

CC The present sequence is that of a colostrinin constituent peptide that is
CC preferred for use as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. Methods are claimed for:
CC inducing a cytokine in a cell by contact with an immunological regulator,
CC where the cell is present in a cell culture, a tissue, an organ or an
CC organism, and the cell is mammalian, including human; modulating an
CC immune response in a cell by contact with the immunological regulator
CC under conditions effective to induce a cytokine; modulating an immune
CC response in a patient by administering an immunological regulator under
CC conditions effective to induce a cytokine, where the immunological
CC regulator is administered topically or as part of a dietary supplement,
CC and where the immune response is specific or non specific, an interferon
CC response or an antibody response; modulating blood cell proliferation by
CC contacting blood cells with a blood cell regulator, where the blood cells
CC are present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patent. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha, interleukin-6 and interleukin-10

XX

SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 5; Length 15;

Best Local Similarity 70.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEVEFPF 14

| | | | |

Db 5 PKLKVEVFPF 14

RESULT 26

AAE20235

ID AAE20235 standard; peptide; 15 AA.

XX

AC AAE20235;

XX

DT 18-JUN-2002 (first entry)

XX

DE Colostrinin constituent peptide #8.

XX

KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnerary.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 15
 FT /note= "Optionally C-terminal amide"
 XX
 PN WO200213850-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022776.
 XX
 PR 17-AUG-2000; 2000WO-US022776.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2002-269151/31.
 XX
 PT Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog.
 XX
 PS Claim 6; Page 25; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress level
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
 CC organ, or organism; or for treating oxidative damage to the skin of a
 CC patient e.g. animal or human; to modulate oxidative stress during/ after
 CC a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide
 XX
 SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 5; Length 15;
 Best Local Similarity 70.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEVPFPF 14
 | | || ||
 Db 5 PKLKVEVPFPF 14

RESULT 27
 ABB09569
 ID ABB09569 standard; peptide; 15 AA.
 XX

AC ABB09569;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Human L1 factor ORF2 associated protein 10.45 N-terminal peptide.
 XX
 KW Human; L1 factor ORF2 associated protein 10.45; open reading frame;
 KW L1 element ORF2-like protein homologue; recombinant production; tumour;
 KW cancer; protein metabolism disorder; cytostatic; gene therapy;
 KW N-terminal peptide; enzyme linked immunosorbent assay; ELISA.
 XX
 OS Homo sapiens.
 XX
 PN CN1338469-A.
 XX
 PD 06-MAR-2002.
 XX
 PF 21-AUG-2000; 2000CN-00119641.
 XX
 PR 21-AUG-2000; 2000CN-00119641.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-384269/42.
 XX
 PT New polypeptide-human L1 factor ORF2 associated protein 10.45 for
 PT treating diseases such as a tumor, or a protein metabolism disorder.
 XX
 PS Example 6; Page 21 (Disclosure); 33pp; Chinese.
 XX
 CC The invention relates to human L1 factor ORF2 associated protein 10.45
 CC (ABB09568) and nucleic acids encoding it (ABL55410). The protein has a
 CC molecular weight of 10.45 kD and has 65% identity and 77% homology over a
 CC 95 amino acid stretch with a human L1 element ORF2-like protein given in
 CC GenBank accession number AF003535. The invention also relates to a method
 CC for the recombinant production of the protein, an antagonist of the
 CC protein, and the use of the protein, gene and antagonist in therapeutic
 CC applications. L1 factor ORF2 associated protein 10.45 can be used in the
 CC treatment of a variety of diseases such as tumours and disorders of
 CC protein metabolism. The present sequence represents the 15 N-terminal
 CC amino acids of human L1 factor ORF2 associated protein 10.45 used in
 CC ELISA (enzyme linked immunosorbent assay) in an exemplification of the
 CC invention
 XX
 SQ Sequence 15 AA;

Query Match 42.0%; Score 34; DB 5; Length 15;
 Best Local Similarity 45.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEPF 12
 |||::|::|
 Db 5 LEKPIVPLQKF 15

RESULT 28

AAB59344

ID AAB59344 standard; peptide; 16 AA.

XX

AC AAB59344;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #4.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 16 AA;

Query Match 42.0%; Score 34; DB 4; Length 16;

Best Local Similarity 70.0%; Pred. No. 1.6e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVL PVE PFPF 14

| | || ||

Db 6 PKL KVE VFPF 15

RESULT 29

AAE34144

ID AAE34144 standard; peptide; 18 AA.

XX

AC AAE34144;

XX

DT 02-MAY-2003 (first entry)

XX

DE T-cell stimulatory gluten peptide #23.

XX

KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;

KW food-related immune enteropathy; tropical sprue; gluten sensitivity;

KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.

XX

OS Unidentified.

XX

PN WO200283722-A2.

XX

PD 24-OCT-2002.

XX

PF 11-APR-2002; 2002WO-NL000235.

XX

PR 12-APR-2001; 2001EP-00201377.

PR 16-NOV-2001; 2001EP-00204383.

XX

PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

XX

PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;

XX

DR WPI; 2003-093000/08.

XX

PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-

PT cell receptor for treating food-related immune enteropathy such as celiac

PT sprue, tropical sprue, giardiasis and food allergies of childhood.

XX

PS Disclosure; Fig 2; 64pp; English.

XX

CC The present invention relates to novel isolated or recombinant human
CC leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional
CC equivalent and/or fragment, capable of recognising a prolamine-derived
CC peptide. The invention relates to recombinant or synthetic prolamine

CC derived peptides involved in food-related immune enteropathy. The
CC pharmaceutical composition is useful to treat food-related immune

CC enteropathies such as celiac sprue, tropical sprue, giardiasis or food
CC allergies of childhood. It is useful to induce tolerance, treat gluten-

CC sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the
CC invention are useful to decrease the amount of toxic prolamine-derived

CC peptides in food or food components and to select and/or breed a cereal.
CC The cereal is useful for inclusion in a diet for a gluten sensitive

CC individual. Blocking substances are useful to decrease the binding of HLA
CC -DQ restricted T-cell receptor to a prolamine-derived peptide involved in

CC food-related immune enteropathy for depletion of T-cells bearing the HLA-
CC DQ restricted T-cell receptor. The present sequence is T-cell stimulatory

CC gluten peptide. This sequence is used in the invention

XX

SQ Sequence 18 AA;

Query Match

42.0%; Score 34; DB 6; Length 18;

Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMPVLPVEFPF 13
: | | ::|||
Db 4 QPYLQLQPF 14

RESULT 30

AAR58339

ID AAR58339 standard; peptide; 14 AA.

XX

AC AAR58339;

XX

DT 22-SEP-1994 (first entry)

XX

DE Hypotensive polypeptide.

XX

KW Hypotensive; antioxidative; calcium absorption; salt; food;
KW pharmaceuticals; physiologically active agents.

XX

OS Lactobacillus helveticus.

XX

PN JP06041191-A.

XX

PD 15-FEB-1994.

XX

PF 03-MAR-1993; 93JP-00043047.

XX

PR 04-MAR-1992; 92JP-00047340.

XX

PA (CALV) CALPIS SHOKUHIN KOGYO KK.

XX

DR WPI; 1994-089332/11.

XX

PT New polypeptide - used in physiologically active agents having e.g.
PT hypotensive antioxidative and calcium absorption promoting activity.

XX

PS Claim 1-2; Page 10; 10pp; Japanese.

XX

CC Sequences (AAR58319-341) are used in conjunction with physiologically
CC active agents showing a property such as hypotensive activity, calcium
CC absorption promoting activity and antioxidative activity. The peptides are
CC non-toxic and can be used in physiologically active agents

XX

SQ Sequence 14 AA;

Query Match 40.7%; Score 33; DB 2; Length 14;

Best Local Similarity 41.7%; Pred. No. 2e+02;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEFP 12
:: | ||:|
Db 3 EMPFPKYPVQPF 14

RESULT 31

AAW85209

ID AAW85209 standard; peptide; 15 AA.

XX

AC AAW85209;

XX

DT 16-FEB-1999 (first entry)

XX

DE Helper T-cell peptide derived from a POL protein.

XX

KW Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;

KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;

KW acquired immune deficiency syndrome; malaria; cancer;

KW allograft rejection; allergy; Lyme disease; hepatitis;

KW post-streptococcal endocarditis; glomerulonephritis;

KW food hypersensitivity.

XX

OS Synthetic.

OS Human immunodeficiency virus 1.

XX

PN WO9832456-A1.

XX

PD 30-JUL-1998.

XX

PF 23-JAN-1998; 98WO-US001373.

XX

PR 23-JAN-1997; 97US-0036713P.

PR 07-FEB-1997; 97US-0037432P.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S;

XX

DR WPI; 1998-427679/36.

XX

PT Composition containing peptide that induces cytotoxic T lymphocyte

PT response, and helper peptide - can bind to human leucocyte antigen

PT alleles, used to treat or prevent cancers, parasitic infections and

PT autoimmune disease.

XX

PS Claim 11; Page 38; 51pp; English.

XX

CC AAW85138-283 represent helper T-cell peptides, which can bind to the

CC human leucocyte antigens (HLA) DR4w4, DR1 and DR7. The peptides are used

CC in the course of the invention. The specification describes peptides that

CC that induce a cytotoxic T lymphocyte (CTL) response, and T-helper

CC peptides, that are used together to generate a CTL response for the

CC treatment or prevention of viral, fungal, bacterial or parasitic

CC infections (e.g. hepatitis, acquired immune deficiency syndrome or

CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate

CC cancer or condyloma acuminatum). Helper T-cell peptides may be used alone

CC to induce a helper T cell response, e.g. in cases of autoimmune disease,

CC allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal

CC endocarditis, glomerulonephritis and food hypersensitivity

XX

SQ Sequence 15 AA;

Query Match

39.5%; Score 32; DB 2; Length 15;

Best Local Similarity 41.7%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEFPF 13
| |:|:| |
Db 4 LNFPISPIETVP 15

RESULT 32

AAW85195

ID AAW85195 standard; peptide; 15 AA.

XX

AC AAW85195;

XX

DT 16-FEB-1999 (first entry)

XX

DE Helper T-cell peptide derived from a POL protein.

XX

KW Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;

KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;

KW acquired immune deficiency syndrome; malaria; cancer;

KW allograft rejection; allergy; Lyme disease; hepatitis;

KW post-streptococcal endocarditis; glomerulonephritis;

KW food hypersensitivity.

XX

OS Synthetic.

OS Human immunodeficiency virus 1.

XX

PN WO9832456-A1.

XX

PD 30-JUL-1998.

XX

PF 23-JAN-1998; 98WO-US001373.

XX

PR 23-JAN-1997; 97US-0036713P.

PR 07-FEB-1997; 97US-0037432P.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S;

XX

DR WPI; 1998-427679/36.

XX

PT Composition containing peptide that induces cytotoxic T lymphocyte

PT response, and helper peptide - can bind to human leucocyte antigen

PT alleles, used to treat or prevent cancers, parasitic infections and

PT autoimmune disease.

XX

PS Claim 11; Page 38; 51pp; English.

XX

CC AAW85138-283 represent helper T-cell peptides, which can bind to the

CC human leucocyte antigens (HLA) DR4w4, DR1 and DR7. The peptides are used

CC in the course of the invention. The specification describes peptides that

CC that induce a cytotoxic T lymphocyte (CTL) response, and T-helper

CC peptides, that are used together to generate a CTL response for the

CC treatment or prevention of viral, fungal, bacterial or parasitic

CC infections (e.g. hepatitis, acquired immune deficiency syndrome or

CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate
CC cancer or condyloma acuminatum). Helper T-cell peptides may be used alone
CC to induce a helper T cell response, e.g. in cases of autoimmune disease,
CC allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal
CC endocarditis, glomerulonephritis and food hypersensitivity

XX

SQ Sequence 15 AA;

Query Match 39.5%; Score 32; DB 2; Length 15;

Best Local Similarity 41.7%; Pred. No. 3.1e+02;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEFPF 13

| | : | : | |

Db 2 LNFPISPIETVP 13

RESULT 33

AAW85329

ID AAW85329 standard; peptide; 15 AA.

XX

AC AAW85329;

XX

DT 16-FEB-1999 (first entry)

XX

DE Helper T-cell class II peptide derived from POL protein.

XX

KW Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;

KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;

KW acquired immune deficiency syndrome; malaria; cancer;

KW allograft rejection; allergy; Lyme disease; hepatitis;

KW post-streptococcal endocarditis; glomerulonephritis;

KW food hypersensitivity.

XX

OS Synthetic.

OS Human immunodeficiency virus 1.

XX

PN WO9832456-A1.

XX

PD 30-JUL-1998.

XX

PF 23-JAN-1998; 98WO-US001373.

XX

PR 23-JAN-1997; 97US-0036713P.

PR 07-FEB-1997; 97US-0037432P.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S;

XX

DR WPI; 1998-427679/36.

XX

PT Composition containing peptide that induces cytotoxic T lymphocyte

PT response, and helper peptide - can bind to human leucocyte antigen

PT alleles, used to treat or prevent cancers, parasitic infections and

PT autoimmune disease.

XX

PS Disclosure; Page 40; 51pp; English.

XX

CC AAW85284-451 represent helper T-cell class II peptides, which can bind to
CC the human leucocyte antigens (HLA) DR4w4, DR1 and DR7. The peptides are
CC used in the course of the invention. The specification describes peptides
CC that that induce a cytotoxic T lymphocyte (CTL) response, and T-helper
CC peptides, that are used together to generate a CTL response for the
CC treatment or prevention of viral, fungal, bacterial or parasitic
CC infections (e.g. hepatitis, acquired immune deficiency syndrome or
CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate
CC cancer or condyloma acuminatum). Helper T-cell peptides may be used alone
CC to induce a helper T cell response, e.g. in cases of autoimmune disease,
CC allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal
CC endocarditis, glomerulonephritis and food hypersensitivity

XX

SQ Sequence 15 AA;

Query Match 39.5%; Score 32; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEFPF 13

| | : | : | |

Db 2 LNFPISPIETVP 13

RESULT 34

ABP24661

ID ABP24661 standard; peptide; 15 AA.

XX

AC ABP24661;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV DR super motif pol peptide #28.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 374; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 15 AA;

Query Match 39.5%; Score 32; DB 4; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEFPF 13
| | : | : |
Db 4 LNFPISPIETVP 15

RESULT 35

ABP24658

ID ABP24658 standard; peptide; 15 AA.

XX

AC ABP24658;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV DR super motif pol peptide #25.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 374; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 15 AA;

Query Match 39.5%; Score 32; DB 4; Length 15;
 Best Local Similarity 41.7%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LEMPVLPVEFPF 13
 | | : | : | |
 Db 2 LNFPISPIETVP 13

RESULT 36
 AAR29099
 ID AAR29099 standard; protein; 16 AA.

XX
 AC AAR29099;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-APR-1993 (first entry)
 XX
 DE Chymotrypsin digestion peptide of p62.
 XX
 KW Guanosine triphosphatase activator protein; GAP; substrate; TK;
 KW tyrosine kinase.
 XX
 OS Homo sapiens.
 XX
 PN WO9220794-A1.
 XX
 PD 26-NOV-1992.
 XX
 PF 14-MAY-1992; 92WO-US004064.
 XX
 PR 17-MAY-1991; 91US-00702771.
 XX
 PA (CETU) CETUS ONCOLOGY CORP.
 XX
 PI Wong GL, McCormick FP;
 XX
 DR WPI; 1992-415772/50.
 XX
 PT Polypeptide P62 which is substrate for tyrosine kinase - also reacts with
 PT the guanosine tri:phosphate activator protein, useful for detecting
 PT cancer.
 XX
 PS Example; Page 37; 50pp; English.
 XX
 CC The p62 was purified from SRD 3T3 cells and the amino acid sequences were
 CC used to generate oligonucleotide probes. The probes were used to screen a
 CC human placental cDNA lambda gt11 library to obtain DNA encoding p62.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 16 AA;

Query Match 39.5%; Score 32; DB 2; Length 16;
 Best Local Similarity 45.5%; Pred. No. 3.3e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EMPVLPVEFP 13
 || ::||: :|
 Db 4 EMVLIPVKQYP 14

RESULT 37
 ADB12816
 ID ADB12816 standard; peptide; 18 AA.
 XX
 AC ADB12816;
 XX
 DT 20-NOV-2003 (first entry)
 XX

DE Antihypertensive peptide #2 for enhancing mineral availability to bones.
 XX
 KW osteopathic; mineral availability; skeletal tissue; casein; osteoporosis;
 KW bone mineral absorption; foodstuff; beverage;
 KW angiotensin converting enzyme; ACE; inhibitor; antihypertensive.
 XX
 OS Unidentified.
 XX
 PN WO2003070267-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 20-DEC-2002; 2002WO-FI001051.
 XX
 PR 25-FEB-2002; 2002FI-00000360.
 XX
 PA (VALI-) VALIO LTD.
 XX
 PI Narva M, Korpela R, Tossavainen O, Maeyrae-Maekinen A;
 XX
 DR WPI; 2003-697569/66.
 XX
 PT Enhancing availability of minerals and treating osteoporosis, comprising
 PT administering small molecular peptides.
 XX
 PS Disclosure; Page 3; 35pp; English.
 XX
 CC The invention relates to enhancing the availability of minerals to
 CC skeletal tissue by administration of casein-derived, small molecular
 CC peptides or a product containing the peptides. The casein-derived, small-
 CC molecular peptide comprises a mixture of short-chain peptides (preferably
 CC di-, tri- or tetra-peptides, especially Ile-Pro-Pro and/or Val-Pro-Pro).
 CC The peptides are useful for enhancing the availability of minerals, in
 CC the treatment of osteoporosis and its pre-stages, for treating disorders
 CC related to mineral availability and bone mineral absorption, and in the
 CC preparation of foodstuff and beverages. This sequence represents an
 CC angiotensin converting enzyme (ACE) inhibitor peptide which is an example
 CC of a biologically active peptide which can be used in the method of the
 CC invention.
 XX
 SQ Sequence 18 AA;

Query Match 38.9%; Score 31.5; DB 6; Length 18;
 Best Local Similarity 50.0%; Pred. No. 4.4e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 3 EMPVLPVE-PFPFV 15
 : ||| | ||| :
 Db 4 QQPVLGVRGPFPII 17

RESULT 38
 AAR93548
 ID AAR93548 standard; peptide; 10 AA.
 XX
 AC AAR93548;
 XX

DT 09-MAY-1996 (first entry)
 XX
 DE Random 10-mer peptide #2 derived from Src SH3 N-terminal.
 XX
 KW SH3 ligand; SH3 binding agent; biased phage library;
 KW recognition sequence; src SH3 domain; Paget's disease; restenosis;
 KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;
 KW p67; complex; chronic myelogenous leukaemia; cancer.
 XX
 OS Synthetic.
 XX
 PN WO9524419-A1.
 XX
 PD 14-SEP-1995.
 XX
 PF 13-MAR-1995; 95WO-US003208.
 XX
 PR 11-MAR-1994; 94US-00209835.
 PR 06-JAN-1995; 95US-00369832.
 XX
 PA (ARIA-) ARIAD PHARM INC.
 XX
 PI Rickles RJ, Brugge JS, Botfield MC, Zoller MJ;
 XX
 DR WPI; 1995-328231/42.
 XX
 PT Identification of peptide(s) binding specifically to SH3 domains - for
 PT use in inhibiting interactions mediated by SH3 domains in treatment of
 PT e.g. osteoporosis and cancer.
 XX
 PS Disclosure; Fig 8; 74pp; English.
 XX
 CC The sequences given in AAR93541-50 represent peptides which are SH3
 CC ligands/SH3 binding agents. They represent a random library based on the
 CC N-terminal peptides of Crk, Lyn, Src and Fyn GST-SH3 fusion proteins.
 CC These sequences were identified using the method of the invention. The
 CC method comprises contacting the SH3 domain with a mixture of peptides
 CC under conditions permitting a ligand to bind to an SH3 domain to form a
 CC complex. Any unbound peptides are removed and the complexed peptide
 CC ligands are dissociated from the complexes. The selected peptides are
 CC enriched by re-contacting them with the SH3 domain and then candidates
 CC which bind to the SH3 domain are detected. The isolated SH3 binding
 CC peptides may be used in the diagnosis, prevention and treatment of
 CC conditions or diseases resulting from cellular processes mediated by an
 CC SH3-based interaction. Such diseases include Paget's disease. Other
 CC conditions treatable with these peptides include restenosis, rheumatoid
 CC arthritis, gout and other problems in which an SH3 of neutrophil oxidase
 CC p47 and p67 complex is implicated, etc
 XX
 SQ Sequence 10 AA;

 Query Match 38.3%; Score 31; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 Qy 7 LPVEPFPPF 14
 ||: |||

Db

3 LPLPPLPF 10

RESULT 39

AAB75678

ID AAB75678 standard; peptide; 10 AA.

XX

AC AAB75678;

XX

DT 10-APR-2001 (first entry)

XX

DE HLA class I binding motif in HOM-TES-84 SEQ ID NO:81.

XX

KW Human; cancer associated antigen precursor; cancer associated antigen;

KW seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;

KW vaccine; cancer.

XX

OS Homo sapiens.

XX

PN WO200100874-A2.

XX

PD 04-JAN-2001.

XX

PF 23-JUN-2000; 2000WO-US017207.

XX

PR 30-JUN-1999; 99US-00346498.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Sahin U, Tureci O, Pfreundschuh M;

XX

DR WPI; 2001-112465/12.

XX

PT Diagnosing a disorder characterized by expression of a human cancer

PT associated antigen precursor, comprises detecting interaction of an agent

PT with a nucleic acid molecule encoding the antigen precursor.

XX

PS Example 10; Page 63; 126pp; English.

XX

CC The present invention describes a method for diagnosing a disorder
CC characterised by expression of a human cancer associated antigen (CAA)
CC precursor (I) coded by a NA Group 1 nucleic acid molecule (N1) comprising
CC contacting the biological sample with an agent (A) that specifically
CC binds to N1, (I) or its fragment, complexed with an human leukocyte
CC antigen (HLA) molecule and determining the interaction between the agent
CC and N1 or (I). (I) has cytostatic activity and can be used in gene
CC therapy and vaccine production. The method can be used for treating a
CC subject with a condition characterised by expression of (I) in cells of a
CC subject. AAB75607 and AAB75608 represent proteins from human cancer
CC associated antigen precursors, and AAB75609 to AAB75802 represent HLA
CC class I binding motifs in human cancer associated antigen precursors
CC given in the exemplification of the present invention

XX

SQ Sequence 10 AA;

Query Match 38.3%; Score 31; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPVEP 11
 |||||
 Db 3 VLPVEP 8

RESULT 40

ABR47334

ID ABR47334 standard; peptide; 10 AA.

XX

AC ABR47334;

XX

DT 10-JUN-2003 (first entry)

XX

DE Staphylococcus aureus CHIPS-related peptide #2523.

XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

KW inflammation; cardiovascular disease; central nervous system disease;

KW gastrointestinal disease; skin disease; genitourinary disease;

KW joint disease; respiratory disease; HIV infection; antiinflammatory;

KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;

KW gynecological; immunosuppressive; anti-HIV.

XX

OS Staphylococcus aureus.

OS Synthetic.

XX

PN WO2003006048-A1.

XX

PD 23-JAN-2003.

XX

PF 11-JUL-2001; 2001WO-EP008004.

XX

PR 11-JUL-2001; 2001WO-EP008004.

XX

PA (JARI-) JARI PHARM BV.

XX

PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;

PI Van Strijp JAG;

XX

DR WPI; 2003-256333/25.

XX

PT Combination of peptides derived from chemotaxis inhibiting protein from

PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases.

XX

PS Example 1; Page 57; 89pp; English.

XX

CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164

CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from

CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX
SQ Sequence 10 AA;

Query Match 38.3%; Score 31; DB 6; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PVEPFP 13
| ||||
Db 2 PFEPFP 7

RESULT 41

ABR47208

ID ABR47208 standard; peptide; 10 AA.

XX

AC ABR47208;

XX

DT 10-JUN-2003 (first entry)

XX

DE Staphylococcus aureus CHIPS-related peptide #2397.

XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

KW inflammation; cardiovascular disease; central nervous system disease;

KW gastrointestinal disease; skin disease; genitourinary disease;

KW joint disease; respiratory disease; HIV infection; antiinflammatory;

KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;

KW gynecological; immunosuppressive; anti-HIV.

XX

OS Staphylococcus aureus.

OS Synthetic.

XX

PN WO2003006048-A1.

XX

PD 23-JAN-2003.

XX

PF 11-JUL-2001; 2001WO-EP008004.

XX

PR 11-JUL-2001; 2001WO-EP008004.

XX

PA (JARI-) JARI PHARM BV.

XX

PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;

PI Van Strijp JAG;

XX

DR WPI; 2003-256333/25.

XX

PT Combination of peptides derived from chemotaxis inhibiting protein from

PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases.

XX

PS Example 1; Page 55; 89pp; English.

XX
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX
SQ Sequence 10 AA;

Query Match 38.3%; Score 31; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EPFPF 14
|||||
Db 4 EPFPF 8

RESULT 42

ABR75157

ID ABR75157 standard; peptide; 12 AA.

XX

AC ABR75157;

XX

DT 28-AUG-2003 (first entry)

XX

DE Elemental carbon-containing molecule affinity peptide SEQ ID NO:10.

XX

KW Biological control; nanoparticle; elemental carbon-containing molecule;

KW biologic scaffold; biologic material binding; organic polymer;

KW cytostatic; synthesis; biosensor; pharmaceutical; cancer.

XX

OS Synthetic.

XX

PN WO2003026590-A2.

XX

PD 03-APR-2003.

XX

PF 27-SEP-2002; 2002WO-US031091.

XX

PR 28-SEP-2001; 2001US-0325664P.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Belcher AM, Smalley RE, Ryan E, Lee S;

XX

DR WPI; 2003-468130/44.

XX

PT Biologic scaffold comprising substrate capable of binding biologic

PT materials, biologic materials, and elemental carbon-containing molecules

PT attached to one or more biologic materials, for treating cancer.

XX

PS Example 4; Fig 1; 160pp; English.

XX

CC The present invention describes a biologic scaffold (I) comprising a
CC substrate capable of binding biologic materials, biologic materials
CC attached to the substrate, and elemental carbon-containing molecules
CC attached to biologic materials or organic polymers. Optionally, (I)
CC comprises a substrate capable of binding bacteriophages, bacteriophages
CC attached to the substrate, peptides that recognise a portion of the
CC bacteriophage, and one or more elemental carbon-containing molecules that
CC recognise the peptide. Biologic scaffold comprising a substrate capable
CC of binding biologic materials, a biologic material attached to the
CC substrate and an organic polymer attached to the biologic material, and
CC elemental carbon-containing molecules attached to the organic polymer.
CC Also described is a molecule (II) comprising, an organic polymer, where
CC the organic polymer selectively recognises and elemental carbon-
CC containing molecule. (I) and (II) have cytostatic activity. (I) and (II)
CC can be used for applications chosen from synthesis of elemental carbon-
CC containing materials, carbon nanotube alignment, creation of biologic
CC semiconductors, junction conversion for single-walled nanotube paste,
CC enhancing solubility and biologic compatibility of single-and multi-
CC walled nanotube paste, producing an integrated single-and multi-walled
CC nanotube paste, biosensor production, release of pharmaceutical
CC compositions, treatment of cancer, and its combinations. ABR75148 to
CC ABR75392 represent peptide sequences used in the exemplification of the
CC present invention

XX

SQ Sequence 12 AA;

Query Match 38.3%; Score 31; DB 6; Length 12;

Best Local Similarity 71.4%; Pred. No. 3.4e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LPVEPFP 13

||: |||

Db 5 LPMTFPF 11

RESULT 43

ADB67069

ID ADB67069 standard; peptide; 12 AA.

XX

AC ADB67069;

XX

DT 04-DEC-2003 (first entry)

XX

DE GaAs binding peptide SEQ ID NO:88.

XX

KW staged assembly; nanostructure; peptide nucleic acid; PNA;

KW structural reinforcement; aerogel; paper; plastic; cement;

KW tensile strength; identification marker; anti-counterfeiting marker;

KW enzyme support; catalyst support; assembly scaffold; nanowire;

KW nanocircuit; molecular sieve; molecular filter; biosensor.

XX

OS Synthetic.

XX

PN WO2003072829-A1.

XX

PD 04-SEP-2003.

XX

PF 21-FEB-2003; 2003WO-US005390.

XX

PR 21-FEB-2002; 2002US-00080608.

XX

PA (NANO-) NANOFRAMES INC.

XX

PI Hyman PL, Goldberg EB;

XX

DR WPI; 2003-721788/68.

XX

PT Staged assembly of nanostructures, useful e.g. in biosensors or as
PT catalyst supports, using assembly units derived from peptide nucleic
PT acids.

XX

PS Disclosure; Page 24; 118pp; English.

XX

CC The present invention describes a method (M1) for the staged assembly of
CC a nanostructure using peptide nucleic acids (PNAs). M1 comprises: (a)
CC contacting a nanostructure intermediate (NSI) having at least one unbound
CC joining element (JE) with an assembly unit (AU) that comprises several
CC different JE where: (i) none of these JE can interact with itself or
CC other JE; and (ii) only one JE in AU and a single unbound JE in NSI are
CC complementary, so that AU becomes non-covalently linked to NSI to produce
CC a new NSI for use in subsequent cycles; (b) removing unbound AU; and (c)
CC cyclic repetition of (a) and (b) to form a nanostructure. The new feature
CC is that the complementary JE in at least one cycle are PNAs. Also
CC described are nanostructures formed from many AU, comprising different
CC JE, where at least one AU includes PNA. M1 is useful for producing
CC nanostructures with a very wide range of potential applications, e.g.
CC structural reinforcements (for aerogels, paper, plastics or cement,
CC particularly as long fibres to improve tensile strength); identification
CC (anti-counterfeiting) markers; enzyme or catalyst supports; assembly
CC scaffolds; for construction of nanowires or nanocircuits; size markers
CC for electron microscopy; molecular sieves and filters; substrates for
CC optical and other surface coatings; scaffolds for solubilising enzymes or
CC for trapping, protecting and delivering specific molecules; in high-
CC density computer memories; as artificial zeolite for absorbing ions from
CC water and for construction of new materials, including use in biosensors.
CC PNAs are more homogeneous than inorganic nanoparticles generally used to
CC form nanostructures, so will produce structures with predictable geometry
CC and stoichiometry. The present sequence represents a peptide which is
CC used in the exemplification of the present invention.

XX

SQ Sequence 12 AA;

Query Match 38.3%; Score 31; DB 7; Length 12;

Best Local Similarity 71.4%; Pred. No. 3.4e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LPVEPFP 13

||: |||

Db 5 LPMTFPF 11

RESULT 44

AA57715

ID AA57715 standard; peptide; 13 AA.

XX

AC AA57715;

XX

DT 14-MAR-2000 (first entry)

XX

DE Human clusterin peptide a.

XX

KW Clusterin; immunosuppressant; organ rejection; tissue transplantation;

KW autoimmune disease; inflammatory disease; rheumatism; atopy;

KW systemic erythematosus; allergy; hay fever.

XX

OS Homo sapiens.

XX

PN WO9962541-A1.

XX

PD 09-DEC-1999.

XX

PF 13-MAY-1999; 99WO-JP002474.

XX

PR 01-JUN-1998; 98JP-00151570.

XX

PA (HISM) HISAMITSU PHARM CO LTD.

XX

PI Yuda K, Akiyama K, Goto T, Goto S;

XX

DR WPI; 2000-072735/06.

XX

PT Immunosuppressants with reduced side-effects, useful for preventing

PT rejection in organ and tissue transplant and as remedies for autoimmune

PT diseases and inflammatory diseases (claimed) e.g. allergy.

XX

PS Example 7; Page 16; 28pp; Japanese.

XX

CC The present invention describes an immunosuppressant which contains a
CC clusterin. The present sequence represents a human clusterin peptide from
CC an example of the present invention. Also described is a method for
CC treating rejection in organ and tissue transplant, autoimmune diseases or
CC inflammatory diseases by administering an effective dose of the
CC immunosuppressant. The immunosuppressants are useful for preventing
CC rejection in organ and tissue transplant, particularly of heart, liver,
CC lung, pancreas, kidney, small intestine, skin and bone marrow, and as
CC remedies for autoimmune diseases such as rheumatism, atopy, systemic
CC erythematosus, and inflammatory diseases including allergy such as hay
CC fever. The drugs are efficacious, with little side-effects

XX

SQ Sequence 13 AA;

Query Match 38.3%; Score 31; DB 3; Length 13;

Best Local Similarity 54.5%; Pred. No. 3.7e+02;

Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 MPVLPVEPFPPF 14

|| | || |

Db 3 MPFSPYEPLNF 13

RESULT 45

AA57716

ID AA57716 standard; peptide; 18 AA.

XX

AC AA57716;

XX

DT 14-MAR-2000 (first entry)

XX

DE Human clusterin peptide alpha.

XX

KW Clusterin; immunosuppressant; organ rejection; tissue transplantation;

KW autoimmune disease; inflammatory disease; rheumatism; atopy;

KW systemic erythematosus; allergy; hay fever.

XX

OS Homo sapiens.

XX

PN WO9962541-A1.

XX

PD 09-DEC-1999.

XX

PF 13-MAY-1999; 99WO-JP002474.

XX

PR 01-JUN-1998; 98JP-00151570.

XX

PA (HISM) HISAMITSU PHARM CO LTD.

XX

PI Yuda K, Akiyama K, Goto T, Goto S;

XX

DR WPI; 2000-072735/06.

XX

PT Immunosuppressants with reduced side-effects, useful for preventing
PT rejection in organ and tissue transplant and as remedies for autoimmune
PT diseases and inflammatory diseases (claimed) e.g. allergy.

XX

PS Example 7; Page 16; 28pp; Japanese.

XX

CC The present invention describes an immunosuppressant which contains a
CC clusterin. The present sequence represents a human clusterin peptide from
CC an example of the present invention. Also described is a method for
CC treating rejection in organ and tissue transplant, autoimmune diseases or
CC inflammatory diseases by administering an effective dose of the
CC immunosuppressant. The immunosuppressants are useful for preventing
CC rejection in organ and tissue transplant, particularly of heart, liver,
CC lung, pancreas, kidney, small intestine, skin and bone marrow, and as
CC remedies for autoimmune diseases such as rheumatism, atopy, systemic
CC erythematosus, and inflammatory diseases including allergy such as hay
CC fever. The drugs are efficacious, with little side-effects

XX

SQ Sequence 18 AA;

Query Match 38.3%; Score 31; DB 3; Length 18;

Best Local Similarity 54.5%; Pred. No. 5.3e+02;

Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 MPVLPVEFPF 14

|| | || |

RESULT 46

ABR25398

ID ABR25398 standard; peptide; 9 AA.

XX

AC ABR25398;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 185P3C3 HLA peptide #1033.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX

PS Claim 13; Page 380; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention

XX

SQ Sequence 9 AA;

Query Match 37.0%; Score 30; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEFPF 13
|::|||
Db 2 PLQFPF 7

RESULT 47

ABR24394

ID ABR24394 standard; peptide; 9 AA.

XX

AC ABR24394;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 185P3C3 HLA peptide #29.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX

PS Claim 13; Page 369; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention

XX

SQ Sequence 9 AA;

Query Match 37.0%; Score 30; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEPPF 13

|::|||

Db 3 PLQPPF 8

RESULT 48

ABR24628

ID ABR24628 standard; peptide; 9 AA.

XX

AC ABR24628;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 185P3C3 HLA peptide #263.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX

PS Claim 13; Page 371; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;

Query Match 37.0%; Score 30; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVEFPF 13
|::|||
Db 2 PLQFPF 7

RESULT 49

ABR25632

ID ABR25632 standard; peptide; 9 AA.

XX

AC ABR25632;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 185P3C3 HLA peptide #1267.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX
 PS Claim 13; Page 383; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 9 AA;

Query Match 37.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEFPF 13
 |::|||
 Db 2 PLQFPF 7

RESULT 50

ABR24838

ID ABR24838 standard; peptide; 9 AA.

XX

AC ABR24838;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 185P3C3 HLA peptide #473.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX

PS Claim 13; Page 374; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention

XX

SQ Sequence 9 AA;

Query Match 37.0%; Score 30; DB 6; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.4e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEPFP 13

|::|||

Db 3 PLQFPF 8

Search completed: July 4, 2004, 04:40:46

Job time : 38.1493 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 9.40299 Seconds
(without alignments)
82.356 Million cell updates/sec

Title: US-09-641-802-5
Perfect score: 81
Sequence: 1 DLEMPVLPVEPFPPFV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7

Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	81	100.0	15	4	US-09-641-803-5	Sequence 5, Appli
2	36	44.4	18	4	US-09-641-803-22	Sequence 22, Appl
3	34	42.0	15	4	US-09-641-803-8	Sequence 8, Appli
4	32	39.5	15	4	US-09-009-953-97	Sequence 97, Appl
5	32	39.5	15	4	US-09-009-953-111	Sequence 111, App
6	32	39.5	16	1	US-07-702-771-5	Sequence 5, Appli
7	32	39.5	16	1	US-08-438-883-5	Sequence 5, Appli
8	32	39.5	16	1	US-08-741-599-5	Sequence 5, Appli
9	31	38.3	8	1	US-08-360-239B-2	Sequence 2, Appli
10	31	38.3	12	4	US-09-914-259-179	Sequence 179, App
11	30	37.0	15	2	US-08-687-956A-8	Sequence 8, Appli

12	30	37.0	15	3	US-08-743-168B-15	Sequence 15, Appl
13	30	37.0	15	5	PCT-US96-10435-15	Sequence 15, Appl
14	30	37.0	16	3	US-08-602-999A-451	Sequence 451, App
15	30	37.0	16	4	US-09-500-124-451	Sequence 451, App
16	29	35.8	13	1	US-08-205-938A-21	Sequence 21, Appl
17	29	35.8	13	5	PCT-US95-02626-21	Sequence 21, Appl
18	29	35.8	14	3	US-08-630-916A-56	Sequence 56, Appl
19	29	35.8	15	2	US-08-687-956A-7	Sequence 7, Appli
20	29	35.8	16	3	US-08-602-999A-202	Sequence 202, App
21	29	35.8	16	3	US-08-602-999A-406	Sequence 406, App
22	29	35.8	16	4	US-09-500-124-202	Sequence 202, App
23	29	35.8	16	4	US-09-500-124-406	Sequence 406, App
24	29	35.8	17	3	US-08-987-743-11	Sequence 11, Appl
25	29	35.8	18	1	US-08-205-938A-22	Sequence 22, Appl
26	29	35.8	18	5	PCT-US95-02626-22	Sequence 22, Appl
27	28	34.6	15	3	US-08-684-187-1	Sequence 1, Appli
28	28	34.6	15	4	US-09-009-953-120	Sequence 120, App
29	28	34.6	16	2	US-08-844-312-9	Sequence 9, Appli
30	28	34.6	17	3	US-08-602-999A-360	Sequence 360, App
31	28	34.6	17	4	US-09-500-124-360	Sequence 360, App
32	28	34.6	18	3	US-08-630-916A-103	Sequence 103, App
33	28	34.6	18	3	US-08-602-999A-317	Sequence 317, App
34	28	34.6	18	4	US-08-630-915A-159	Sequence 159, App
35	28	34.6	18	4	US-09-500-124-317	Sequence 317, App
36	27	33.3	8	3	US-08-828-712-12	Sequence 12, Appl
37	27	33.3	8	3	US-08-993-165-25	Sequence 25, Appl
38	27	33.3	8	3	US-08-993-165-28	Sequence 28, Appl
39	27	33.3	8	3	US-08-993-165-30	Sequence 30, Appl
40	27	33.3	8	3	US-09-063-276-12	Sequence 12, Appl
41	27	33.3	8	4	US-09-540-448-25	Sequence 25, Appl
42	27	33.3	8	4	US-09-540-448-28	Sequence 28, Appl
43	27	33.3	8	4	US-09-496-761-1	Sequence 1, Appli
44	27	33.3	8	4	US-09-496-761-4	Sequence 4, Appli
45	27	33.3	8	4	US-09-496-761-6	Sequence 6, Appli
46	27	33.3	8	4	US-09-324-782-12	Sequence 12, Appl
47	27	33.3	8	4	US-09-668-143-12	Sequence 12, Appl
48	27	33.3	8	4	US-08-913-612A-46	Sequence 46, Appl
49	27	33.3	8	4	US-08-929-847-26	Sequence 26, Appl
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51	27	33.3	9	3	US-08-828-712-13	Sequence 13, Appl
52	27	33.3	9	3	US-08-828-712-14	Sequence 14, Appl
53	27	33.3	9	3	US-09-063-276-13	Sequence 13, Appl
54	27	33.3	9	3	US-09-063-276-14	Sequence 14, Appl
55	27	33.3	9	4	US-09-324-782-13	Sequence 13, Appl
56	27	33.3	9	4	US-09-324-782-14	Sequence 14, Appl
57	27	33.3	9	4	US-09-668-143-13	Sequence 13, Appl
58	27	33.3	9	4	US-09-668-143-14	Sequence 14, Appl
59	27	33.3	9	4	US-08-913-612A-47	Sequence 47, Appl
60	27	33.3	10	1	US-08-214-650-40	Sequence 40, Appl
61	27	33.3	10	4	US-09-051-380-16	Sequence 16, Appl
62	27	33.3	14	3	US-09-208-966-11	Sequence 11, Appl
63	27	33.3	14	4	US-09-775-052A-11	Sequence 11, Appl
64	27	33.3	14	6	5164482-18	Patent No. 5164482
65	27	33.3	15	1	US-08-230-047-27	Sequence 27, Appl
66	27	33.3	15	3	US-08-602-999A-467	Sequence 467, App
67	27	33.3	15	4	US-09-500-124-467	Sequence 467, App
68	27	33.3	15	4	US-09-647-372B-74	Sequence 74, Appl

69	27	33.3	16	2	US-08-844-312-10	Sequence 10, Appl
70	27	33.3	16	3	US-08-602-999A-200	Sequence 200, App
71	27	33.3	16	3	US-08-602-999A-220	Sequence 220, App
72	27	33.3	16	4	US-09-500-124-200	Sequence 200, App
73	27	33.3	16	4	US-09-500-124-220	Sequence 220, App
74	27	33.3	17	4	US-08-469-260A-251	Sequence 251, App
75	27	33.3	17	4	US-08-488-446-251	Sequence 251, App
76	27	33.3	17	4	US-08-467-344A-251	Sequence 251, App
77	27	33.3	17	4	US-09-428-082B-272	Sequence 272, App
78	27	33.3	18	2	US-08-374-652C-90	Sequence 90, Appl
79	26.5	32.7	15	4	US-09-205-258-379	Sequence 379, App
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82	26	32.1	8	1	US-08-360-239B-1	Sequence 1, Appli
83	26	32.1	8	3	US-08-993-165-34	Sequence 34, Appl
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85	26	32.1	8	4	US-09-496-761-10	Sequence 10, Appl
86	26	32.1	8	4	US-08-929-847-34	Sequence 34, Appl
87	26	32.1	9	3	US-08-993-165-29	Sequence 29, Appl
88	26	32.1	9	4	US-09-540-448-29	Sequence 29, Appl
89	26	32.1	9	4	US-09-496-761-5	Sequence 5, Appli
90	26	32.1	9	4	US-08-929-847-30	Sequence 30, Appl
91	26	32.1	10	1	US-08-230-047-13	Sequence 13, Appl
92	26	32.1	11	1	US-08-336-343A-32	Sequence 32, Appl
93	26	32.1	11	2	US-08-630-645-20	Sequence 20, Appl
94	26	32.1	11	3	US-08-652-877-33	Sequence 33, Appl
95	26	32.1	11	3	US-08-476-515A-33	Sequence 33, Appl
96	26	32.1	11	4	US-08-766-596A-20	Sequence 20, Appl
97	26	32.1	11	5	PCT-US96-10220-20	Sequence 20, Appl
98	26	32.1	12	2	US-08-459-568-61	Sequence 61, Appl
99	26	32.1	12	2	US-08-399-411-61	Sequence 61, Appl
100	26	32.1	12	3	US-08-516-859A-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1

US-09-641-803-5

; Sequence 5, Application US/09641803

; Patent No. 6500798

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

; FILE REFERENCE: 265.00220101

; CURRENT APPLICATION NUMBER: US/09/641,803

; CURRENT FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: 60/149,310

; PRIOR FILING DATE: 1999-08-17

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-5

Query Match 100.0%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPFPPFV 15
|||||||
Db 1 DLEMPVLPVEPFPPFV 15

RESULT 2

US-09-641-803-22

; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-22

Query Match 44.4%; Score 36; DB 4; Length 18;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
:: | ||||
Db 3 EMPFPKYPVEPF 14

RESULT 3

US-09-641-803-8

; Sequence 8, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.

```
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-8
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Query Match          42.0%; Score 34; DB 4; Length 15;
Best Local Similarity 70.0%; Pred. No. 34;
Matches      7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      5 PVLPVEPFPPF 14
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Db      5 PKLKVEVFPF 14
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RESULT 4

US-09-009-953-97

; Sequence 97, Application US/09009953

; Patent No. 6413517

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; TITLE OF INVENTION: Identification of Broadly

; Reactive DR Restricted Epitopes

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,953

; FILING DATE: 21-Jan-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,713

; FILING DATE: 23-JAN-1997

; APPLICATION NUMBER: US 60/037,432

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;          FILING DATE: 07-FEB-1997
;  ATTORNEY/AGENT INFORMATION:
;          NAME: Weber, Ellen Lauver
;          REGISTRATION NUMBER: 32,762
;          REFERENCE/DOCKET NUMBER: 018623-011520US
;  TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 415-576-0200
;          TELEFAX: 415-576-0300
;          TELEX: <Unknown>
;  INFORMATION FOR SEQ ID NO: 97:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 15 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: peptide
;    SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-009-953-97

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Query Match          39.5%;  Score 32;  DB 4;  Length 15;
Best Local Similarity 41.7%;  Pred. No. 69;
Matches      5;  Conservative      2;  Mismatches      5;  Indels      0;  Gaps      0;

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Qy      2 LEMPVLPVEFPF 13
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Db      2 LNFPISPIETVP 13

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RESULT 5

US-09-009-953-111

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; Sequence 111, Application US/09009953
; Patent No. 6413517

```

GENERAL INFORMATION:

```

;  APPLICANT: Sette, Alessandro
;  TITLE OF INVENTION: Identification of Broadly
;                      Reactive DR Restricted Epitopes
;  NUMBER OF SEQUENCES: 274
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Townsend and Townsend and Crew LLP
;    STREET: Two Embarcadero Center, Eighth Floor
;    CITY: San Francisco
;    STATE: CA
;    COUNTRY: USA
;    ZIP: 94111-3834
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Diskette
;    COMPUTER: IBM Compatible
;    OPERATING SYSTEM: DOS
;    SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/09/009,953
;    FILING DATE: 21-Jan-1998
;    CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 60/036,713
;    FILING DATE: 23-JAN-1997
;    APPLICATION NUMBER: US 60/037,432

```

```

;          FILING DATE: 07-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Weber, Ellen Lauver
;          REGISTRATION NUMBER: 32,762
;          REFERENCE/DOCKET NUMBER: 018623-011520US
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 415-576-0200
;          TELEFAX: 415-576-0300
;          TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 111:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 15 amino acids
;        TYPE: amino acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-009-953-111

```

```

Query Match          39.5%;  Score 32;  DB 4;  Length 15;
Best Local Similarity 41.7%;  Pred. No. 69;
Matches      5;  Conservative      2;  Mismatches      5;  Indels      0;  Gaps      0;

```

```

QY          2 LEMPVLPVEFPF 13
             |  | :  | : |  |
Db          4 LNFPISPIETVP 15

```

RESULT 6

US-07-702-771-5

```

; Sequence 5, Application US/07702771
; Patent No. 5610276
;  GENERAL INFORMATION:
;    APPLICANT: Wong, Gail L.
;    APPLICANT: McCormick, Frank
;    TITLE OF INVENTION: Cloning and Purification of P62
;    NUMBER OF SEQUENCES: 10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Cetus Corporation
;      STREET: 1400 Fifty-Third Street
;      CITY: Emeryville
;      STATE: California
;      ZIP: 94608-2997
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/07/702,771
;      FILING DATE: 17-MAY-1991
;      CLASSIFICATION: 435
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Giotta, Gregory J.
;      REGISTRATION NUMBER: 32,028
;      REFERENCE/DOCKET NUMBER: 2594
;    TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 415-420-3300
; TELEFAX: 415-658-5239
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-07-702-771-5

Query Match 39.5%; Score 32; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 73;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EMPVLPVEFPF 13
|| ::||: :|
Db 4 EMVLIPVKQYP 14

RESULT 7

US-08-438-883-5

; Sequence 5, Application US/08438883
; Patent No. 5731427
; GENERAL INFORMATION:
; APPLICANT: Wong, G.
; APPLICANT: McCormick, F.
; TITLE OF INVENTION: Purification and Cloning of p62
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,883
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/702,771
; FILING DATE: 17-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 27527/33275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: N
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-438-883-5

Query Match 39.5%; Score 32; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 73;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EMPVLPVEFPF 13
|| ::||: :|
Db 4 EMVLIPVKQYP 14

RESULT 8

US-08-741-599-5

; Sequence 5, Application US/08741599
; Patent No. 5773237
; GENERAL INFORMATION:
; APPLICANT: Wong, G.
; APPLICANT: McCormick, F.
; TITLE OF INVENTION: Purification and Cloning of p62
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,599
; FILING DATE: 01-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/702,771
; FILING DATE: 17-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 0892.003/33583
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448

; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: N
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-741-599-5

Query Match 39.5%; Score 32; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 73;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EMPVLPVEFPF 13
|| ::||: :|
Db 4 EMVLIPVKQYP 14

RESULT 9

US-08-360-239B-2

; Sequence 2, Application US/08360239B
; Patent No. 5801222
; GENERAL INFORMATION:
; APPLICANT: Pettit, George R.
; APPLICANT: Tan, Rui
; TITLE OF INVENTION: Isolation and Structure of
; TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic
; TITLE OF INVENTION: Octapeptides Phakellistatin 10 and 11
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Mybeck
; STREET: 8010 East Morgan Trail, #10
; CITY: Scottsdale
; STATE: Arizona
; COUNTRY: USA
; ZIP: 85258-1234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,239B
; FILING DATE: 12/20/94
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard R. Mybeck
; REGISTRATION NUMBER: 17,886
; REFERENCE/DOCKET NUMBER: 4997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (602)-483-1285
; TELEFAX: (602)-483-7452
; INFORMATION FOR SEQ ID NO: 2:


```
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acid residues
;   TYPE: amino acid
;   TOPOLOGY: Cyclic
; MOLECULE TYPE:
;   DESCRIPTION: Cyclooctapeptide
;   DESCRIPTION: phakellistatin 11
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: circular
; ORIGINAL SOURCE:
;   ORGANISM: Phakellia sp.
;   DEVELOPMENTAL STAGE: whole organism
; FEATURE:
;   NAME/KEY: phakellistatin 11
;   NAME/KEY: amino acid analysis, high resolution
;   NAME/KEY: nuclear magnetic resonance and mass
;   NAME/KEY: spectral MS/MS techniques
;   OTHER INFORMATION: Phakellistatin is a
;   OTHER INFORMATION: cell growth inhibitory peptide with
;   OTHER INFORMATION: activity in murine lymphocytic leukemia
;   OTHER INFORMATION: cell line of 0.20 mg/ml.
```

US-08-360-239B-2

```
Query Match          38.3%;  Score 31;  DB 1;  Length 8;
Best Local Similarity 66.7%;  Pred. No. 3e+05;
Matches      4;  Conservative      2;  Mismatches      0;  Indels      0;  Gaps      0;
```

```
Qy      10 EPFPFV 15
        :||||:
Db      2 QPFPFI 7
```

RESULT 10

US-09-914-259-179

```
; Sequence 179, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Identified from M13 bacteriophage peptide display
library.
```

US-09-914-259-179

```
Query Match          38.3%;  Score 31;  DB 4;  Length 12;
```

Best Local Similarity 71.4%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LPVEFPF 13
||: |||
Db 5 LPMTFPF 11

RESULT 11

US-08-687-956A-8

; Sequence 8, Application US/08687956A

; Patent No. 5861157

; GENERAL INFORMATION:

; APPLICANT: BURNIE, JAMES P

; APPLICANT: MATTHEWS, RUTH C

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP

; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH

; STREET: FLOOR

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/687,956A

; FILING DATE: 29-JUL-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9401689.6

; FILING DATE: 28-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: KOKULIS, PAUL N

; REGISTRATION NUMBER: 16,773

; REFERENCE/DOCKET NUMBER: 50885/222892

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202/861-3000

; TELEFAX: 202/822-0944

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; ORGANISM: Streptococcus sobrinus

; STRAIN: Streptococcus sobrinus MUCOB 263

US-08-687-956A-8

Query Match 37.0%; Score 30; DB 2; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEP 11
| :| |||
Db 4 DQNIPDKPVEP 14

RESULT 12

US-08-743-168B-15

; Sequence 15, Application US/08743168B

; Patent No. 6271015

; GENERAL INFORMATION:

; APPLICANT: Gilula, No. 6271015ton B

; APPLICANT: Cravatt, Benjamin F

; APPLICANT: Lerner, Richard A

; TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute

; STREET: 10550 No. 6271015th Torrey Pines Road

; CITY: La Jolla

; STATE: California

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/743,168B

; FILING DATE: 04-NOV-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/489,535

; FILING DATE: 12-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: TSRI 485.2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 784-2937

; TELEFAX: (619) 784-9399

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-743-168B-15

Query Match 37.0%; Score 30; DB 3; Length 15;

Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 5 PVLPVEPFPPF 14
| :| |||
Db 5 PTVP--PFPP 12

RESULT 13

PCT-US96-10435-15

; Sequence 15, Application PC/TUS9610435

; GENERAL INFORMATION:

; APPLICANT: The Scripps Research Institute

; TITLE OF INVENTION: CIS-9, 10-OCTADECENOAMIDASE

; NUMBER OF SEQUENCES: 32

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/10435

; FILING DATE: 12-JUN-1996

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/489,535

; FILING DATE: 12-JUN-1995

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

PCT-US96-10435-15

Query Match 37.0%; Score 30; DB 5; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 5 PVLPVEPFPPF 14
| :| |||
Db 5 PTVP--PFPP 12

RESULT 14

US-08-602-999A-451

; Sequence 451, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

```

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 451:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-451

```

```

Query Match          37.0%; Score 30; DB 3; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches      4; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 PVLPEP 11
        |:|::|
Db      6 PLLPIKP 12

```

RESULT 15

US-09-500-124-451

```

; Sequence 451, Application US/09500124
; Patent No. 6432920

```

GENERAL INFORMATION:

```

; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

```

```

; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 451:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-451

```

```

Query Match          37.0%; Score 30; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches      4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 PVLPVEP 11
        |:|:|:|
Db      6 PLLPIKP 12

```

RESULT 16

US-08-205-938A-21

; Sequence 21, Application US/08205938A

; Patent No. 5466671

; GENERAL INFORMATION:

; APPLICANT: TEMPST, PAUL

; APPLICANT: CASTEELS, PETER

; TITLE OF INVENTION: APIDAECIN-TYPE PEPTIDE ANTIBIOTICS WITH

; TITLE OF INVENTION: IMPROVED ACTIVITIES AND/OR DIFFERENT

; TITLE OF INVENTION: ANTIBACTERIAL SPECTRUM

; NUMBER OF SEQUENCES: 43

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: COOPER & DUNHAM LLP
;   STREET: 1185 AVENUE OF THE AMERICAS
;   CITY: NEW YORK
;   STATE: NEW YORK
;   COUNTRY: USA
;   ZIP: 10036
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.24
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/205,938A
;   FILING DATE: 02-MAR-1994
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;   NAME: WHITE, JOHN P
;   REGISTRATION NUMBER: 28,678
;   REFERENCE/DOCKET NUMBER: 45061
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)278-0400
;   TELEFAX: (212) 391-0525
;   INFORMATION FOR SEQ ID NO: 21:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 13 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-205-938A-21

```

```

Query Match          35.8%; Score 29; DB 1; Length 13;
Best Local Similarity 36.4%; Pred. No. 1.7e+02;
Matches      4; Conservative      4; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      3 EMPVLPVEFPF 13
        ::|: | :| |
Db      1 QVPIRPSQPRP 11

```

```

RESULT 17
PCT-US95-02626-21
; Sequence 21, Application PC/TUS9502626
; GENERAL INFORMATION:
;   APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
;   APPLICANT: TEMPST, PAUL
;   APPLICANT: CASTEELS, PETER
;   TITLE OF INVENTION: APIDAECIN-TYPE PEPTIDE ANTIBIOTICS WITH IMPROVED
;   TITLE OF INVENTION: ACTIVITIES AND/OR DIFFERENT ANTIBACTERIAL SPECTRUM
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: COOPER & DUNHAM LLP
;   STREET: 1185 AVENUE OF THE AMERICAS
;   CITY: NEW YORK
;   STATE: NEW YORK
;   COUNTRY: USA
;   ZIP: 10036

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02626
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,938
; FILING DATE: 02-MAR-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45061-A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-02626-21

```

```

Query Match          35.8%; Score 29; DB 5; Length 13;
Best Local Similarity 36.4%; Pred. No. 1.7e+02;
Matches      4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      3 EMPVLPVEFPF 13
        ::||:|:|:|
Db      1 QVPIRPSQPRP 11

```

RESULT 18

US-08-630-916A-56

; Sequence 56, Application US/08630916A

; Patent No. 6011137

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; APPLICANT: Kay, Brian K.

; APPLICANT: Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING
SAME

; NUMBER OF SEQUENCES: 124

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States

; ZIP: 10036-2711

; COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-56

```

```

Query Match          35.8%; Score 29; DB 3; Length 14;
Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches      5; Conservative 1; Mismatches      5; Indels      0; Gaps      0;

```

```

Qy      3 EMPVLPVEFPF 13
        | | | |:|
Db      1 EYPPYPPPPYP 11

```

RESULT 19

US-08-687-956A-7

```

; Sequence 7, Application US/08687956A
; Patent No. 5861157
; GENERAL INFORMATION:
; APPLICANT: BURNIE, JAMES P
; APPLICANT: MATTHEWS, RUTH C
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
; STREET: FLOOR
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/687,956A
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401689.6
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 50885/222892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/861-3000
; TELEFAX: 202/822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus sobrinus
; STRAIN: Streptococcus sobrinus MUCOB 263
US-08-687-956A-7

```

```

Query Match          35.8%; Score 29; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches      6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      3 EMPVLPVEP 11
        |: |||||
Db      6 ELVDLPVEP 14

```

RESULT 20

US-08-602-999A-202

```

; Sequence 202, Application US/08602999A
; Patent No. 6184205

```

GENERAL INFORMATION:

```

; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```

```

;      ZIP: 10036-2711
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/602,999A
;      FILING DATE: 16-FEB-1996
;      CLASSIFICATION: 435
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Misrock, S. Leslie
;      REGISTRATION NUMBER: 18,872
;      REFERENCE/DOCKET NUMBER: 1101-202
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 790-9090
;      TELEFAX: (212) 869-9741/8864
;      TELEX: 66141 PENNIE
;      INFORMATION FOR SEQ ID NO: 202:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 16 amino acids
;      TYPE: amino acid
;      TOPOLOGY: unknown
;      MOLECULE TYPE: peptide
US-08-602-999A-202

```

```

Query Match          35.8%; Score 29; DB 3; Length 16;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches      6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1 DLEMPVLP 8
        | | | | |
Db      3 DPERPVLP 10

```

RESULT 21

```

US-08-602-999A-406
; Sequence 406, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 406:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-406

```

```

Query Match          35.8%; Score 29; DB 3; Length 16;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches      5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 LEMPVLP 8
        |::|||
Db      4 LKLPVLP 10

```

RESULT 22

US-09-500-124-202

```

; Sequence 202, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 202:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-202

```

```

Query Match          35.8%; Score 29; DB 4; Length 16;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches      6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1 DLEMPVLP 8
        | | |||
Db      3 DPERPVLP 10

```

RESULT 23

US-09-500-124-406

```

; Sequence 406, Application US/09500124
; Patent No. 6432920

```

GENERAL INFORMATION:

```

; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```

```

;      ZIP: 10036-2711
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/500,124
;      FILING DATE:
;      CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/602,999
;      FILING DATE: 16-FEB-1996
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Misrock, S. Leslie
;      REGISTRATION NUMBER: 18,872
;      REFERENCE/DOCKET NUMBER: 1101-202
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 790-9090
;      TELEFAX: (212) 869-9741/8864
;      TELEX: 66141 PENNIE
;      INFORMATION FOR SEQ ID NO: 406:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 16 amino acids
;      TYPE: amino acid
;      TOPOLOGY: unknown
;      MOLECULE TYPE: peptide
US-09-500-124-406

```

```

Query Match          35.8%; Score 29; DB 4; Length 16;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches      5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 LEMPVLP 8
        |::|||
Db      4 LKLPVLP 10

```

RESULT 24

US-08-987-743-11

; Sequence 11, Application US/08987743

; Patent No. 6123938

; GENERAL INFORMATION:

; APPLICANT: Stern, Robert

; APPLICANT: Csoka, Anthony

; APPLICANT: Frost, Gregory I.

; APPLICANT: Wong, Tim M.

; TITLE OF INVENTION: Purification and Microsequencing of

; TITLE OF INVENTION: Hylauronidase Isozymes

; FILE REFERENCE: 9076/088CIP2

; CURRENT APPLICATION NUMBER: US/08/987,743

; CURRENT FILING DATE: 1997-12-09

; EARLIER APPLICATION NUMBER: 08/733,360

; EARLIER FILING DATE: 1996-10-17

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 11

; LENGTH: 17
; TYPE: PRT
; ORGANISM: H. sapiens
US-08-987-743-11

Query Match 35.8%; Score 29; DB 3; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PVLPEVEPFV 15
|:| | |
Db 4 PLLPNXPFTTV 14

RESULT 25

US-08-205-938A-22

; Sequence 22, Application US/08205938A
; Patent No. 5466671

; GENERAL INFORMATION:

; APPLICANT: TEMPST, PAUL
; APPLICANT: CASTEELS, PETER
; TITLE OF INVENTION: APIDAECIN-TYPE PEPTIDE ANTIBIOTICS WITH
; TITLE OF INVENTION: IMPROVED ACTIVITIES AND/OR DIFFERENT
; TITLE OF INVENTION: ANTIBACTERIAL SPECTRUM
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/205,938A
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45061

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)278-0400
; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-205-938A-22

Query Match 35.8%; Score 29; DB 1; Length 18;

Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMPVLPVEFPF 13
::|: | :| |
Db 6 QVPIRPSQPRP 16

RESULT 26

PCT-US95-02626-22

; Sequence 22, Application PC/TUS9502626

; GENERAL INFORMATION:

; APPLICANT: SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH

; APPLICANT: TEMPST, PAUL

; APPLICANT: CASTEELS, PETER

; TITLE OF INVENTION: APIDAECIN-TYPE PEPTIDE ANTIBIOTICS WITH IMPROVED

; TITLE OF INVENTION: ACTIVITIES AND/OR DIFFERENT ANTIBACTERIAL SPECTRUM

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: COOPER & DUNHAM LLP

; STREET: 1185 AVENUE OF THE AMERICAS

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/02626

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/205,938

; FILING DATE: 02-MAR-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: WHITE, JOHN P

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 45061-A-PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

PCT-US95-02626-22

Query Match 35.8%; Score 29; DB 5; Length 18;

Best Local Similarity 36.4%; Pred. No. 2.4e+02;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMPVLPVEFPF 13
::|: | :| |
Db 6 QVPIRPSQPRP 16

RESULT 27

US-08-684-187-1

; Sequence 1, Application US/08684187A
; Patent No. 6020171
; GENERAL INFORMATION:
; APPLICANT: SAITO, ATSUSHI
; APPLICANT: SHINAGAWA, HIDEO
; APPLICANT: NAKATA, ATSUO
; TITLE OF INVENTION: METHOD OF PREPARING PLASMID HAVING BOTH EXPRESSING
; TITLE OF INVENTION: ABILITY OF RETROVIRAL GENE AND PROCESSING ABILITY AFTER
; TITLE OF INVENTION: TRANSLATION, AND RESULTANT PLASMID AND EXPRESSION
; TITLE OF INVENTION: PRODUCTS THEREOF
; FILE REFERENCE: 96-0747/lc(wmc)/653
; CURRENT APPLICATION NUMBER: US/08/684,187A
; CURRENT FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: N-TERMINAL
; OTHER INFORMATION: AMINO ACID SEQUENCE

US-08-684-187-1

Query Match 34.6%; Score 28; DB 3; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEFPF 13
|: |:| |
Db 1 PISPIETVP 9

RESULT 28

US-09-009-953-120

; Sequence 120, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; Reactive DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:

```

;           MEDIUM TYPE: Diskette
;           COMPUTER: IBM Compatible
;           OPERATING SYSTEM: DOS
;           SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/009,953
;           FILING DATE: 21-Jan-1998
;           CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 60/036,713
;           FILING DATE: 23-JAN-1997
;           APPLICATION NUMBER: US 60/037,432
;           FILING DATE: 07-FEB-1997
;   ATTORNEY/AGENT INFORMATION:
;           NAME: Weber, Ellen Lauver
;           REGISTRATION NUMBER: 32,762
;           REFERENCE/DOCKET NUMBER: 018623-011520US
;   TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 415-576-0200
;           TELEFAX: 415-576-0300
;           TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 120:
;           SEQUENCE CHARACTERISTICS:
;           LENGTH: 15 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;           MOLECULE TYPE: peptide
;           SEQUENCE DESCRIPTION: SEQ ID NO: 120:
US-09-009-953-120

```

```

Query Match          34.6%;  Score 28;  DB 4;  Length 15;
Best Local Similarity 44.4%;  Pred. No. 2.8e+02;
Matches      4;  Conservative      2;  Mismatches      3;  Indels      0;  Gaps      0;

```

```

Qy      5 PVLPEPFP 13
        |: |:| |
Db      3 PISPIETVP 11

```

RESULT 29

US-08-844-312-9

; Sequence 9, Application US/08844312

; Patent No. 5948639

; GENERAL INFORMATION:

; APPLICANT: Carlos J. Gimeno and Dean A. Falb

; TITLE OF INVENTION: No. 5948639e1 TGF-{SYMBOL 98 \f "Symbol"} Pathway

Genes

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,312
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-844-312-9

```

```

Query Match          34.6%; Score 28; DB 2; Length 16;
Best Local Similarity 38.5%; Pred. No. 2.9e+02;
Matches      5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy      1 DLEMPVLPVEFPF 13
        :|| | | :|
Db      4 ELESPPAPYSRYP 16

```

RESULT 30

US-08-602-999A-360

```

; Sequence 360, Application US/08602999A
; Patent No. 6184205

```

; GENERAL INFORMATION:

```

; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```

```

;      ZIP: 10036-2711
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/602,999A
;      FILING DATE: 16-FEB-1996
;      CLASSIFICATION: 435
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Misrock, S. Leslie
;      REGISTRATION NUMBER: 18,872
;      REFERENCE/DOCKET NUMBER: 1101-202
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 790-9090
;      TELEFAX: (212) 869-9741/8864
;      TELEX: 66141 PENNIE
;      INFORMATION FOR SEQ ID NO: 360:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 17 amino acids
;      TYPE: amino acid
;      TOPOLOGY: unknown
;      MOLECULE TYPE: peptide
US-08-602-999A-360

```

```

Query Match          34.6%; Score 28; DB 3; Length 17;
Best Local Similarity 45.5%; Pred. No. 3.1e+02;
Matches      5; Conservative 1; Mismatches      5; Indels      0; Gaps      0;

```

```

Qy      4 MPVLPVEPFPPF 14
        :| | | ||
Db      4 LPPPPPPPLPF 14

```

RESULT 31

US-09-500-124-360

; Sequence 360, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-360

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Query Match          34.6%; Score 28; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 3.1e+02;
Matches      5; Conservative 1; Mismatches      5; Indels      0; Gaps      0;

```

```

Qy      4 MPVLPVEPF 14
        :| | | |
Db      4 LPPPPPPPLPF 14

```

RESULT 32

US-08-630-916A-103

; Sequence 103, Application US/08630916A

; Patent No. 6011137

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; APPLICANT: Kay, Brian K.

; APPLICANT: Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING
SAME

; NUMBER OF SEQUENCES: 124

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-103

```

```

Query Match          34.6%; Score 28; DB 3; Length 18;
Best Local Similarity 30.8%; Pred. No. 3.3e+02;
Matches      4; Conservative      5; Mismatches      4; Indels      0; Gaps      0;

```

```

Qy      3 EMPVLPVEPFPPFV 15
        ::| :| :| | :
Db      6 QLPPVPPKPRPLL 18

```

RESULT 33

US-08-602-999A-317

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; Sequence 317, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,999A
;      FILING DATE:  16-FEB-1996
;      CLASSIFICATION:  435
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  1101-202
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;      INFORMATION FOR SEQ ID NO:  317:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;      MOLECULE TYPE:  peptide
US-08-602-999A-317

```

```

Query Match          34.6%;  Score 28;  DB 3;  Length 18;
Best Local Similarity 30.8%;  Pred. No. 3.3e+02;
Matches      4;  Conservative      5;  Mismatches      4;  Indels      0;  Gaps      0;

```

```

Qy      3 EMPVLPVEPFPPFV 15
        ::| :| :| | :
Db      6 QLPPVPPKPRPLL 18

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RESULT 34

US-08-630-915A-159

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; Sequence 159, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  HOFFMAN, No. 6309820h
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  FOWLKES, Dana M.
;   APPLICANT:  McCONNELL, Stephen J.
;   TITLE OF INVENTION:  POLYPEPTIDES HAVING A FUNCTIONAL
;   TITLE OF INVENTION:  DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
;   TITLE OF INVENTION:  USING SAME
;   NUMBER OF SEQUENCES:  227
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds LLP
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  USA
;   ZIP:  10036-2711
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS

```

```

;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/630,915A
;   FILING DATE:  03-APR-1996
;   CLASSIFICATION:  536
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Misrock, S. Leslie
;   REGISTRATION NUMBER:  18,872
;   REFERENCE/DOCKET NUMBER:  1101-174
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 869-8864/9741
;   TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  159:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  18 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:
;   TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-08-630-915A-159

```

```

Query Match          34.6%;  Score 28;  DB 4;  Length 18;
Best Local Similarity 30.8%;  Pred. No. 3.3e+02;
Matches      4;  Conservative      5;  Mismatches      4;  Indels      0;  Gaps      0;

```

```

Qy      3 EMPVLPVEPFPPFV 15
        ::| :| :| | :
Db      6 QLPPVPPKPRPLL 18

```

RESULT 35

US-09-500-124-317

```

; Sequence 317, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  THORN, Judith M.
;   APPLICANT:  QUILLIAM, Lawrence A.
;   APPLICANT:  DER, Channing J.
;   APPLICANT:  FOWLKES, Dana M.
;   APPLICANT:  RIDER, James E.
;   TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;   TITLE OF INVENTION:  ISOLATING AND USING SAME
;   NUMBER OF SEQUENCES:  467
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS

```



```

;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/500,124
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/602,999
;   FILING DATE:  16-FEB-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Misrock, S. Leslie
;   REGISTRATION NUMBER:  18,872
;   REFERENCE/DOCKET NUMBER:  1101-202
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 869-9741/8864
;   TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  317:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  18 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-09-500-124-317

```

```

Query Match          34.6%;  Score 28;  DB 4;  Length 18;
Best Local Similarity 30.8%;  Pred. No. 3.3e+02;
Matches      4;  Conservative      5;  Mismatches      4;  Indels      0;  Gaps      0;

```

```

Qy      3 EMPVLPVEPFPPFV 15
        ::| :| :| | :
Db      6 QLPPVPPKPRPLL 18

```

RESULT 36

US-08-828-712-12

```

; Sequence 12, Application US/08828712
; Patent No. 6015884
; GENERAL INFORMATION:
;   APPLICANT:  Schneck, Jonathan P.
;   APPLICANT:  O'Herrin, Sean
;   TITLE OF INVENTION:  Soluble Divalent and Multivalent
;   TITLE OF INVENTION:  Heterodimeric Analogs of Proteins
;   NUMBER OF SEQUENCES:  20
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Banner & Witcoff, Ltd.
;   STREET:  1001 G Street, N.W.
;   CITY:  Washington
;   STATE:  D.C.
;   COUNTRY:  U.S.A.
;   ZIP:  20001
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/828,712

```

; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.73713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)508-9100
; TELEFAX: (202)508-9299
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide p2Ca
US-08-828-712-12

Query Match 33.3%; Score 27; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
: ||||
Db 1 LSPFPF 6

RESULT 37

US-08-993-165-25
; Sequence 25, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yunqiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el
Sequence
US-08-993-165-25

Query Match 33.3%; Score 27; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14

: ||||
Db 1 LSPFPF 6

RESULT 38

US-08-993-165-28

; Sequence 28, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yunqiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el
Sequence
US-08-993-165-28

Query Match 33.3%; Score 27; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
 : ||||
Db 1 LSPFPF 6

RESULT 39

US-08-993-165-30

; Sequence 30, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yunqiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el
Sequence
US-08-993-165-30

Query Match 33.3%; Score 27; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
: ||||
Db 1 LSPFPF 6

RESULT 40

US-09-063-276-12

; Sequence 12, Application US/09063276
; Patent No. 6140113
; GENERAL INFORMATION:
; APPLICANT: Schneck, Jonathan
; APPLICANT: O'Herrin, Sean
; TITLE OF INVENTION: Molecular Complexes Which
; TITLE OF INVENTION: Modify Immune Responses
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,276
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,712
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: 60/014,367
; FILING DATE: 28-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.74154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6140113e
US-09-063-276-12

Query Match 33.3%; Score 27; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
: ||||
Db 1 LSPFPF 6

RESULT 41

US-09-540-448-25

; Sequence 25, Application US/09540448
; Patent No. 6403056
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/09/540,448
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056e1
Sequence
US-09-540-448-25

Query Match 33.3%; Score 27; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
: ||||
Db 1 LSPFPF 6

RESULT 42

US-09-540-448-28

; Sequence 28, Application US/09540448
; Patent No. 6403056
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/09/540,448
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el
Sequence
US-09-540-448-28

Query Match 33.3%; Score 27; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
: ||||
Db 1 LSPFPF 6

RESULT 43

US-09-496-761-1

; Sequence 1, Application US/09496761
; Patent No. 6444660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, De Kang
; TITLE OF INVENTION: No. 6444660el Lipid Soluble Steroid Prodrugs
; FILE REFERENCE: UNGR-1586
; CURRENT APPLICATION NUMBER: US/09/496,761
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/851,780
; PRIOR FILING DATE: 1997-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-496-761-1

Query Match 33.3%; Score 27; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
: ||||
Db 1 LSPFPF 6

RESULT 44

US-09-496-761-4

; Sequence 4, Application US/09496761
; Patent No. 6444660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, De Kang
; TITLE OF INVENTION: No. 6444660el Lipid Soluble Steroid Prodrugs
; FILE REFERENCE: UNGR-1586

; CURRENT APPLICATION NUMBER: US/09/496,761
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/851,780
; PRIOR FILING DATE: 1997-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-496-761-4

Query Match 33.3%; Score 27; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
: ||||
Db 1 LSPFPF 6

RESULT 45

US-09-496-761-6

; Sequence 6, Application US/09496761
; Patent No. 6444660
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; APPLICANT: Shen, De Kang
; TITLE OF INVENTION: No. 6444660el Lipid Soluble Steroid Prodrugs
; FILE REFERENCE: UNGR-1586
; CURRENT APPLICATION NUMBER: US/09/496,761
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 08/851,780
; PRIOR FILING DATE: 1997-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-496-761-6

Query Match 33.3%; Score 27; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
: ||||
Db 1 LSPFPF 6

RESULT 46

US-09-324-782-12

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; Sequence 12, Application US/09324782
; Patent No. 6448071
; GENERAL INFORMATION:
;   APPLICANT:  Schneck, Jonathan P.
;   APPLICANT:  O'Herrin, Sean
;   TITLE OF INVENTION:  Soluble Divalent and Multivalent
;   TITLE OF INVENTION:  Heterodimeric Analogs of Proteins
;   NUMBER OF SEQUENCES:  20
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Banner & Witcoff, Ltd.
;     STREET:    1001 G Street, N.W.
;     CITY:      Washington
;     STATE:     D.C.
;     COUNTRY:   U.S.A.
;     ZIP:       20001
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/324,782
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/828,712
;     FILING DATE:  28-MAR-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Kagan, Sarah A.
;     REGISTRATION NUMBER:  32,141
;     REFERENCE/DOCKET NUMBER:  01107.73713
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (202)508-9100
;     TELEFAX:   (202)508-9299
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:    amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE:  peptide p2Ca
US-09-324-782-12

```

```

Query Match          33.3%;  Score 27;  DB 4;  Length 8;
Best Local Similarity 66.7%;  Pred. No. 3e+05;
Matches      4;  Conservative    1;  Mismatches    1;  Indels      0;  Gaps      0;

```

```

Qy          9 VEPFPF 14
              : ||||
Db          1 LSPFPF 6

```

```

RESULT 47
US-09-668-143-12

```



```

; Sequence 12, Application US/09668143
; Patent No. 6458354
; GENERAL INFORMATION:
;   APPLICANT:  Schneck, Jonathan P.
;   APPLICANT:  O'Herrin, Sean
;   TITLE OF INVENTION:  Soluble Divalent and Multivalent
;   TITLE OF INVENTION:  Heterodimeric Analogs of Proteins
;   NUMBER OF SEQUENCES:  20
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Banner & Witcoff, Ltd.
;     STREET:  1001 G Street, N.W.
;     CITY:  Washington
;     STATE:  D.C.
;     COUNTRY:  U.S.A.
;     ZIP:  20001
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/668,143
;     FILING DATE:  25-SEP-2000
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/828,712
;     FILING DATE:  28-MAR-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Kagan, Sarah A.
;     REGISTRATION NUMBER:  32,141
;     REFERENCE/DOCKET NUMBER:  01107.73713
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (202)508-9100
;     TELEFAX:  (202)508-9299
;   INFORMATION FOR SEQ ID NO: 12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE:  peptide p2Ca
US-09-668-143-12

```

```

Query Match          33.3%;  Score 27;  DB 4;  Length 8;
Best Local Similarity 66.7%;  Pred. No. 3e+05;
Matches      4;  Conservative    1;  Mismatches    1;  Indels      0;  Gaps      0;

```

```

Qy          9 VEPFPF 14
              : ||||
Db          1 LSPFPF 6

```

```

RESULT 48
US-08-913-612A-46
; Sequence 46, Application US/08913612A

```

```

; Patent No. 6461867
; GENERAL INFORMATION:
;   APPLICANT: Cai, Zeling
;   APPLICANT: Sprent, Jonathan
;   APPLICANT: Brunmark, Anders
;   APPLICANT: Jackson, Michael
;   APPLICANT: Peterson, Per A.
;   TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
;   TITLE OF INVENTION: ACTIVATION OF T-CELLS
;   NUMBER OF SEQUENCES: 65
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Olson & Hierl, Ltd.
;     STREET: 20 No. 6461867th Wacker Drive, 36th Floor
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: USA
;     ZIP: 60606
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/913,612A
;     FILING DATE: 08-SEP-1997
;     CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Cepuritis, Talivaldis
;     REGISTRATION NUMBER: 20,818
;     REFERENCE/DOCKET NUMBER: 471.1 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (312) 580-1180
;     TELEFAX: (312) 580-1189
;   INFORMATION FOR SEQ ID NO: 46:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 8 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: internal
US-08-913-612A-46

```

```

Query Match          33.3%; Score 27; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches      4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      9 VEPFPF 14
        : ||||
Db      1 LSPFPF 6

```

```

RESULT 49
US-08-929-847-26
; Sequence 26, Application US/08929847

```

```

; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled
Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-26

```

```

Query Match          33.3%; Score 27; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches      4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      9 VEPFPF 14
        : ||||
Db      1 LSPFPF 6

```

RESULT 50

```

US-08-929-847-29
; Sequence 29, Application US/08929847
; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled
Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-29

```

```

Query Match          33.3%; Score 27; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches      4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      9 VEPFPF 14
        : ||||
Db      1 LSPFPF 6

```

Search completed: July 4, 2004, 04:48:48
Job time : 10.403 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 11.5299 Seconds
(without alignments)
125.142 Million cell updates/sec

Title: US-09-641-802-5
Perfect score: 81
Sequence: 1 DLEMPVLPVEPFPPFV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7

Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	27	33.3	17	2	S59481	hydroxyproline-ric
2	25	30.9	11	2	I33098	173K exoantigen -
3	25	30.9	15	2	B39109	hypothetical 1.5K
4	24	29.6	15	2	PS0455	superoxide dismuta
5	24	29.6	15	2	PA0088	protein QF200051 -
6	24	29.6	17	2	G85956	hypothetical prote
7	23	28.4	16	2	PC4371	telomeric and tetr
8	22.5	27.8	17	2	S17274	ribosomal protein
9	22	27.2	11	2	A55149	tetracenomycin A2
10	22	27.2	14	2	B56884	Pax-QNR, long form
11	22	27.2	14	2	G33160	H+-transporting tw
12	22	27.2	15	2	PA0060	protein QF200037 -
13	22	27.2	16	2	E58503	superoxide dismuta

14	22	27.2	16	2	A23992	melatin-ommochrome
15	22	27.2	18	2	S56715	hydroxymethylgluta
16	22	27.2	18	2	S29166	quinaldine oxidore
17	21	25.9	9	2	S66419	tetrameric protein
18	21	25.9	15	2	S20410	protein kinase (EC
19	21	25.9	15	2	PS0452	32K protein 3306 -
20	21	25.9	16	2	A20190	hypodermin B - ear
21	21	25.9	17	2	A49237	45/47K antigen - M
22	21	25.9	17	2	E23734	insulin-like growt
23	21	25.9	18	2	A28060	elastase inhibitor
24	21	25.9	18	2	I78841	thrombopoietin rec
25	20	24.7	9	2	S66635	alpha-2-macroglobu
26	20	24.7	10	2	B59272	peptide-N4-(N-acet
27	20	24.7	11	2	PA0028	protein QA300042 -
28	20	24.7	11	2	PN0042	stathmin - mouse (
29	20	24.7	13	2	S21152	tryptophyllin-rela
30	20	24.7	13	2	B47415	mannose-1-phosphat
31	20	24.7	14	2	H64008	hypothetical prote
32	20	24.7	15	2	PA0024	protein QA300050 -
33	20	24.7	16	1	A49761	locustapyrokinin -
34	20	24.7	16	2	A60551	leukocyte elastase
35	20	24.7	18	2	A42576	steroid receptor c
36	20	24.7	18	2	I52614	u-plasminogen acti
37	20	24.7	18	2	A28027	protein P2 - curle
38	20	24.7	18	2	A40760	basic fibroblast g
39	19	23.5	10	2	B61218	alpha-gliadin 6Ha
40	19	23.5	11	2	PQ0231	beta-glucosidase (
41	19	23.5	13	2	A05174	tryptophyllin-13 -
42	19	23.5	13	2	A59387	VCAM-1 5'UTR bindi
43	19	23.5	15	2	S29207	avenin gamma-4 - o
44	19	23.5	15	2	I40665	ilvBN leader pepti
45	19	23.5	15	2	PA0026	protein QA300027 -
46	19	23.5	15	2	A41436	alpha-macroglobuli
47	19	23.5	15	2	C61511	milk band B protei
48	19	23.5	16	2	T37075	hypothetical prote
49	19	23.5	16	2	A45454	ankyrin-binding gl
50	19	23.5	17	2	JQ2030	hypothetical 1.9K
51	19	23.5	17	2	I55612	thyroid hormone re
52	19	23.5	17	4	I51887	hypothetical EWSR1
53	19	23.5	18	2	S04229	N4-(beta-N-acetylgl
54	19	23.5	18	2	I51427	hemoglobin alpha c
55	19	23.5	18	2	PN0149	beta-Gliadine 13 -
56	19	23.5	18	2	A60915	enkephalin-degradi
57	19	23.5	18	2	A54651	insulin-like growt
58	18	22.2	9	2	A60356	118K stomach cance
59	18	22.2	9	2	S26508	collagen alpha 2.(V
60	18	22.2	10	2	B33710	ornithine decarbox
61	18	22.2	10	2	S18396	probable glucose-6
62	18	22.2	11	2	S21727	gamma-interferon-i
63	18	22.2	11	2	A54348	N-acetylglucosamin
64	18	22.2	12	2	S67528	napin - rape (frag
65	18	22.2	12	2	S70344	amine oxidase (cop
66	18	22.2	14	2	S21247	H+-transporting tw
67	18	22.2	14	2	A60158	disaggregatase - M
68	18	22.2	14	2	PL0152	metal-binding prot
69	18	22.2	15	2	PA0071	superoxide dismuta
70	18	22.2	15	2	A56963	acid phosphatase (

71	18	22.2	16	2	C45133	casein kinase II (
72	18	22.2	16	2	PA0048	protein QA100047 -
73	18	22.2	16	2	B23692	transcription fact
74	18	22.2	17	2	I49593	cystic fibrosis tr
75	18	22.2	17	2	I84733	gene CFTR protein
76	18	22.2	18	2	S29264	ovohemerythrin - d
77	18	22.2	18	2	S09722	2S albumin small c
78	18	22.2	18	2	S09723	2S albumin small c
79	18	22.2	18	2	S71592	serine proteinase
80	18	22.2	18	2	A39040	calsequestrin, car
81	18	22.2	18	2	I46653	T-cell receptor de
82	17.5	21.6	15	2	A54397	ubiquitin-carrier
83	17	21.0	7	2	ECMUCR	catch-relaxing pep
84	17	21.0	8	2	S16324	hypothetical prote
85	17	21.0	8	2	A46306	spasmogenic toxin
86	17	21.0	8	2	S10783	enamelin f - bovin
87	17	21.0	9	2	S13636	coat protein beta
88	17	21.0	9	2	A61620	locustamyotropin I
89	17	21.0	9	2	PC7074	translation elonga
90	17	21.0	10	2	A60624	angiotensin I - Ja
91	17	21.0	10	2	A90917	angiotensin precur
92	17	21.0	10	2	A90345	angiotensin precur
93	17	21.0	11	1	XAVIBH	bradykinin-potenti
94	17	21.0	11	2	S07207	Crinia-angiotensin
95	17	21.0	11	2	PC2254	cytochrome P450 3A
96	17	21.0	12	2	C36201	1-aminocyclopropan
97	17	21.0	12	2	S01749	collagen alpha 1(I
98	17	21.0	12	2	E45691	probable minor cap
99	17	21.0	12	2	A61503	sterol carrier pro
100	17	21.0	12	2	S74196	3-hydroxy-3-methyl

ALIGNMENTS

RESULT 1

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C;Species: Phaseolus vulgaris (kidney bean)

C;Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998

C;Accession: S59481

R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A;Title: Specificity in the immobilisation of cell wall proteins in response to different elicitor molecules in suspension-cultured cells of French bean (Phaseolus vulgaris L.).

A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59481

A;Molecule type: protein

A;Residues: 1-17 <WOJ>

C;Keywords: glycoprotein; hydroxyproline

F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 33.3%; Score 27; DB 2; Length 17;

Best Local Similarity 46.7%; Pred. No. 2.6e+02;

Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DLEMPVLPVEPFPPFV 15
 |: :| || | | |
 Db 1 DMYLP--PVPPPPVV 13

RESULT 2

I33098

173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C;Accession: I33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: I33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIC>

Query Match 30.9%; Score 25; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 3.4e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EMPVLPV 9
 |:|: |:
 Db 5 ELPLFPI 11

RESULT 3

B39109

hypothetical 1.5K protein - hepatitis C virus

N;Alternate names: hypothetical protein 2

C;Species: hepatitis C virus

C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999

C;Accession: B39109; JQ1585

R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.;
 Tekamp-Olson, P.; Kuo, G.; Choo, Q.L.; Houghton, M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

A;Title: Characterization of the terminal regions of hepatitis C viral RNA:
 identification of conserved sequences in the 5' untranslated region and poly(A)
 tails at the 3' end.

A;Reference number: A39109; MUID:91156678; PMID:1705704

A;Accession: B39109

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-15 <HAN>

A;Cross-references: GB:M58406

R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.
 J. Gen. Virol. 73, 1521-1525, 1992

A;Title: Cloning and sequencing of the structural region and expression of
 putative core gene of hepatitis C virus from a British case of chronic sporadic
 hepatitis.

A;Reference number: JQ1584; MUID:92300349; PMID:1318944

A;Accession: JQ1585

A;Molecule type: genomic RNA

A;Residues: 1-15 <KUM>

A;Experimental source: strain U.K.

Query Match 30.9%; Score 25; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVLPVEP 11
| |||
Db 9 PPLPGEP 15

RESULT 4

PS0455

superoxide dismutase (EC 1.15.1.1) (Mn) - rice (strain Nihonbare) (fragment)

C;Species: Oryza sativa (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Mar-1999

C;Accession: PS0455

R;Tsugita, A.

submitted to JIPID, April 1993

A;Reference number: PS0206

A;Accession: PS0455

A;Molecule type: protein

A;Residues: 1-15 <TSU>

A;Experimental source: germ

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen and hydrogen peroxide

C;Keywords: metalloprotein; oxidoreductase

Query Match 29.6%; Score 24; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 7e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MPVLPVE 10
:|:|:| :
Db 6 LPILPYD 12

RESULT 5

PA0088

protein QF200051 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0088

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichisides proteins.

A;Reference number: PA0051

A;Accession: PA0088

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 29.6%; Score 24; DB 2; Length 15;
Best Local Similarity 27.3%; Pred. No. 7e+02;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EMPVLPVEFPF 13

: | :| : :|
Db 1 QKPDIPXDDYP 11

RESULT 6

G85956

hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: G85956

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: G85956

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-17 <STO>

A;Cross-references: GB:AE005174; NID:g12517539; PIDN:AAG58115.1; GSPDB:GN00145; UWGP:Z4331

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z4331

Query Match 29.6%; Score 24; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFP 13

 | | |

Db 4 VSPFP 8

RESULT 7

PC4371

telomeric and tetraplex DNA binding protein qTBP42 I - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999

C;Accession: PC4371

R;Sarig, G.; Weisman-Shomer, P.; Fry, M.

Biochem. Biophys. Res. Commun. 237, 617-623, 1997

A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CARG box binding protein CBF-A.

A;Reference number: PC4371; MUID:97445086; PMID:9299414

A;Accession: PC4371

A;Molecule type: protein

A;Residues: 1-16 <SAR>

C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular or bimolecular tetraplex forms of the telomeric G-strand.

Query Match 28.4%; Score 23; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEP 11
 ||||
 Db 5 PVEP 8

RESULT 8

S17274

ribosomal protein YmL35, mitochondrial, questionable - yeast (*Saccharomyces cerevisiae*) (fragment)

C;Species: *Saccharomyces cerevisiae*

A;Variety: strain 07173

C;Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997

C;Accession: S17274

R;Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.

FEBS Lett. 284, 51-56, 1991

A;Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria.

A;Reference number: S17255; MUID:91285106; PMID:2060626

A;Accession: S17274

A;Molecule type: protein

A;Residues: 1-17 <GRO>

C;Comment: A coding region for this protein could not be identified in the genome of *Saccharomyces cerevisiae* S288C.

C;Genetics:

A;Genome: nuclear

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 27.8%; Score 22.5; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 7 LPVEP-FPFV 15
 || :| :| |
 Db 8 LPTDPVYPXV 17

RESULT 9

A55149

tetracenomycin A2 oxygenase (EC 1.-.-.-) - *Streptomyces glaucescens* (fragment)

N;Alternate names: tcmA2 oxygenase; tcmG

C;Species: *Streptomyces glaucescens*

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Mar-1996

C;Accession: A55149

R;Shen, B.; Hutchinson, C.R.

J. Biol. Chem. 269, 30726-30733, 1994

A;Title: Triple hydroxylation of tetracenomycin A2 to tetracenomycin C in *Streptomyces glaucescens*. Overexpression of the tcmG gene in *Streptomyces lividans* and characterization of the tetracenomycin A2 oxygenase.

A;Reference number: A55149; MUID:95074090; PMID:7982994

A;Accession: A55149

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <SHE>

C;Genetics:

A;Start codon: TTG

C;Keywords: antibiotic biosynthesis; FAD; monomer; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EMPVLPV 9
|:| | | |
Db 5 EVPVLIV 11

RESULT 10

B56884

Pax-QNR, long form - quail (fragment)

C;Species: Coturnix coturnix (quail)

C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 21-Jul-2000

C;Accession: B56884

R;Dozier, C.; Carriere, C.; Grevin, D.; Martin, P.; Quatannens, B.; Stehelin, D.; Saule, S.

Cell Growth Differ. 4, 281-289, 1993

A;Title: Structure and DNA-binding properties of Pax-QNR, a paired box- and homeobox-containing gene.

A;Reference number: A56884; MUID:93264300; PMID:8098617

A;Accession: B56884

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-14 <DOZ>

A;Cross-references: GB:X68169; NID:g311558; PIDN:CAA48271.1; PID:g311559

A;Experimental source: neuroretina cells

C;Keywords: alternative splicing; retina

Query Match 27.2%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PVLPEPF 12
| | | |
Db 1 PTPVSSF 8

RESULT 11

G33160

H+-transporting two-sector ATPase (EC 3.6.3.14) 9K chain - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 03-Jun-2002

C;Accession: G33160

R;Godinot, C.

submitted to the Protein Sequence Database, February 1991

A;Reference number: A33160

A;Accession: G33160

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <GOD>

C;Keywords: hydrolase

Query Match 27.2%; Score 22; DB 2; Length 14;

Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 VLPVEPFPPV 15
| ||: | :
Db 1 VXPVQVSPLI 10

RESULT 12

PA0060

protein QF200037 - fungus (*Fusarium sporotrichioides*) (fragment)

C;Species: *Fusarium sporotrichioides*

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0060

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides* proteins.

A;Reference number: PA0051

A;Accession: PA0060

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PVEPFP 13
|: ||
Db 1 PLRPLP 6

RESULT 13

E58503

superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)

N;Alternate names: 21.3K bladder and kidney stone protein

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 05-Mar-1999

C;Accession: E58503

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: E58503

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <BIN>

A;Experimental source: human bladder and kidney stones

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen and hydrogen peroxide

C;Keywords: metalloprotein; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MPVLPVE 10
:| || |
Db 5 LPPLPYE 11

RESULT 14

A23992

melatin-ommochrome-stimulating hormone III - silkworm (fragment)

N;Alternate names: melanization and reddish coloration hormone III; MRCH III

C;Species: Bombyx mori (silkworm)

C;Date: 30-Jan-1988 #sequence_revision 30-Jan-1988 #text_change 18-Jun-1993

C;Accession: A23992

R;Matsumoto, S.; Isogai, A.; Suzuki, A.

FEBS Lett. 189, 115-118, 1985

A;Title: N-terminal amino acid sequence of an insect neurohormone, melanization and reddish coloration hormone (MRCH): heterogeneity and sequence homology with human insulin-like growth factor II.

A;Reference number: A23992; MUID:85285612; PMID:3896851

A;Accession: A23992

A;Molecule type: protein

A;Residues: 1-16 <MAT>

C;Keywords: hormone

Query Match 27.2%; Score 22; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EMPVLPVE 10
:|| | :
Db 5 DMPATPAD 12

RESULT 15

S56715

hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) (clone hmg3.2) - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 03-Jun-2002

C;Accession: S56715

R;Bhattacharyya, M.K.; Paiva, N.L.; Dixon, R.A.; Korth, K.L.; Stermer, B.A.

Plant Mol. Biol. 28, 1-15, 1995

A;Title: Features of the hmg 1 subfamily of genes encoding HMG-CoA reductase in potato.

A;Reference number: S56710; MUID:95306778; PMID:7787174

A;Accession: S56715

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-18 <BHA>

A;Cross-references: EMBL:L34830; NID:g529524; PIDN:AAC37437.1; PID:g553101

C;Superfamily: hydroxymethylglutaryl-CoA reductase (NADPH)

C;Keywords: coenzyme A; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVLPEP 11

Db || |: |
7 PVKPLYP 13

RESULT 16

S29166

quinaldine oxidoreductase (EC 1.5.99.-) beta chain - *Arthrobacter* sp. (isolate Rue 61a) (fragment)

C;Species: *Arthrobacter* sp.

A;Variety: isolate Rue 61a

C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C;Accession: S29166

R;de Beyer, A.; Lingens, F.

Biol. Chem. Hoppe-Seyler 374, 101-110, 1993

A;Title: Microbial metabolism of quinoline and related compounds. XVI.

Quinaldine oxidoreductase from *Arthrobacter* spec. Rue 61a: a molybdenum-containing enzyme catalysing the hydroxylation at C-4 of the heterocycle.

A;Reference number: S29165; MUID:93228843; PMID:8471177

A;Accession: S29166

A;Molecule type: protein

A;Residues: 1-18 <BEY>

A;Experimental source: isolate Rue 61a

C;Complex: heterohexamer; two alpha, two beta and two gamma chains

C;Function:

A;Description: catalyzes the oxidation of quinaldine to 1H-4-oxoquinaldine

A;Pathway: quinaldine degradation

C;Keywords: FAD; flavoprotein; heterohexamer; molybdopterin; oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 VEPFPFV 15

: || |:

Db 2 MHPFQFI 8

RESULT 17

S66419

tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)

C;Species: *Spinacia oleracea* (spinach)

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997

C;Accession: S66419

R;Kuwabara, T.

FEBS Lett. 371, 195-198, 1995

A;Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spinach thylakoids: structural similarities between the protease and polyphenol oxidase.

A;Reference number: S66419; MUID:95402209; PMID:7672127

A;Accession: S66419

A;Molecule type: protein

A;Residues: 1-9 <KUW>

Query Match 25.9%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLP 8
|:|
Db 2 PILP 5

RESULT 18

S20410

protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)

N;Alternate names: LHCI protein kinase

C;Species: chloroplast *Spinacia oleracea* (spinach)

C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C;Accession: S20410

R;Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.

FEBS Lett. 298, 33-35, 1992

A;Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome complex.

A;Reference number: S20410; MUID:92183823; PMID:1544419

A;Accession: S20410

A;Molecule type: protein

A;Residues: 1-15 <GAL>

C;Genetics:

A;Genome: chloroplast

C;Function:

A;Description: is responsible for the regulation of energy distribution between photosystem I and II

A;Note: does not exhibit redox-controlled activation

C;Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphotransferase; photosynthesis; thylakoid

Query Match 25.9%; Score 21; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLP 8
|:|
Db 2 PILP 5

RESULT 19

PS0452

32K protein 3306 - rice (strain Nihonbare) (fragment)

C;Species: *Oryza sativa* (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C;Accession: PS0452

R;Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993

A;Reference number: PS0208

A;Accession: PS0452

A;Molecule type: protein

A;Residues: 1-15 <TSU>

A;Experimental source: bran, strain Nihonbare

C;Comment: molecular weight 32K, pI 5.3.

Query Match 25.9%; Score 21; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PFPFV 15
||| :
Db 6 PFPIL 10

RESULT 20

A20190

hypodermin B - early cattle grub (fragment)

C;Species: Hypoderma lineatum (early cattle grub)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Jun-1993

C;Accession: A20190

R;Lecroisey, A.; Tong, N.T.; Keil, B.

Eur. J. Biochem. 134, 261-267, 1983

A;Title: Hypodermin B, a trypsin-related enzyme from the insect Hypoderma lineatum.

A;Reference number: A20190; MUID:83261874; PMID:6307690

A;Accession: A20190

A;Molecule type: protein

A;Residues: 1-16 <LEC>

Query Match 25.9%; Score 21; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPP 14
:| ||:
Db 9 IEDFPW 14

RESULT 21

A49237

45/47K antigen - Mycobacterium bovis (fragment)

C;Species: Mycobacterium bovis

C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995

C;Accession: A49237

R;Romain, F.; Laqueyrie, A.; Militzer, P.; Pescher, P.; Chavarot, P.;

Lagranderie, M.; Auregan, G.; Gheorghiu, M.; Marchal, G.

Infect. Immun. 61, 742-750, 1993

A;Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex, an immunodominant target for antibody response after immunization with living bacteria.

A;Reference number: A49237; MUID:93138802; PMID:8423100

A;Contents: BCG

A;Accession: A49237

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <ROM>

A;Note: sequence extracted from NCBI backbone (NCBIP:123246)

Query Match 25.9%; Score 21; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEP 11
| |||
Db 4 PAPPVPP 10

RESULT 22

E23734

insulin-like growth factor-binding protein 3 - pig (fragment)

C;Species: *Sus scrofa domestica* (domestic pig)

C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993

C;Accession: E23734

R;Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.

Mol. Endocrinol. 5, 938-948, 1991

A;Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6.

A;Reference number: A23734; MUID:92049376; PMID:1719383

A;Accession: E23734

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <SHI>

Query Match 25.9%; Score 21; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVLPEP 11

||: ||

Db 9 PVVRXEP 15

RESULT 23

A28060

elastase inhibitor, leukocyte - horse (fragment)

C;Species: *Equus caballus* (domestic horse)

C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 15-Sep-2003

C;Accession: A28060

R;Potempa, J.; Dubin, A.; Watorek, W.; Travis, J.

J. Biol. Chem. 263, 7364-7369, 1988

A;Title: An elastase inhibitor from equine leukocyte cytosol belongs to the serpin superfamily. Further characterization and amino acid sequence of the reactive center.

A;Reference number: A28060; MUID:88213423; PMID:3366785

A;Accession: A28060

A;Molecule type: protein

A;Residues: 1-18 <POT>

C;Superfamily: Serpin

Query Match 25.9%; Score 21; DB 2; Length 18;
Best Local Similarity 35.7%; Pred. No. 2.6e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

Qy 6 VLPVEPF----PFV 15

::| | | ||:

Db 4 LMPEENFNADHPFI 17

RESULT 24

I78841

thrombopoietin receptor - mouse (fragment)

C;Species: *Mus sp.* (mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I78841
R;Alexander, W.S.; Dunn, A.R.
Oncogene 10, 795-803, 1995
A;Title: Structure and transcription of the genomic locus encoding murine c-Mpl,
a receptor for thrombopoietin.
A;Reference number: I58350; MUID:95166571; PMID:7862460
A;Accession: I78841
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-18 <RES>
A;Cross-references: GB:S76842; NID:g912990; PIDN:AAB33462.1; PID:g912991
C;Genetics:
A;Gene: c-mp11

Query Match 25.9%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PVEPFPPV 15
| | ||:
Db 2 PHGPAPFL 9

RESULT 25

S66635

alpha-2-macroglobulin isoform 1 - bovine (fragment)

C;Species: Bos primigenius indicus (zebu cattle)

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66635

R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup,
S.; Sottrup-Jensen, L.; Nyborg, J.

FEBS Lett. 372, 93-95, 1995

A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding
domain of human and bovine alpha(2)-macroglobulin.

A;Reference number: S66634; MUID:96032553; PMID:7556651

A;Accession: S66635

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <DOL>

Query Match 24.7%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EPFPF 14
: |||
Db 2 DEFPPF 6

RESULT 26

B59272

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small
chain - sweet almond (fragment)

N;Alternate names: peptide N-glycosidase

C;Species: Prunus dulcis var. sativa (sweet almond)

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000

C;Accession: B59272
R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminy)asparagine
amidase A and its N-glycans.
A;Reference number: A59272; MUID:98181894; PMID:9523720
A;Accession: B59272
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ALT>
C;Keywords: hydrolase

Query Match 24.7%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PVEFP 13
|: ||
Db 4 PLHDFP 9

RESULT 27

PA0028

protein QA300042 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C;Accession: PA0028

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-
dimensional gel electrophoresis.

A;Reference number: PA0001

A;Accession: PA0028

A;Molecule type: protein

A;Residues: 1-11 <KAM>

A;Experimental source: seed

C;Keywords: seed

Query Match 24.7%; Score 20; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFP 13
|||
Db 6 PFP 8

RESULT 28

PN0042

stathmin - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998

C;Accession: PN0042

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of
mouse neuroblastoma cells.

A;Reference number: PN0041
A;Accession: PN0042
A;Molecule type: protein
A;Residues: 1-11 <KAT>
A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 17,500 and the pI is 5.63. The amino-terminus is blocked.
C;Keywords: brain

Query Match 24.7%; Score 20; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 2.2e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MPVLPVEP 11
:| |:|
Db 3 VPDFPLSP 10

RESULT 29

S21152

tryptophyllin-related peptide - two-colored leaf frog

C;Species: Phyllomedusa bicolor (two-colored leaf frog)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S21152

R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.; Barra, D.

FEBS Lett. 302, 151-154, 1992

A;Title: Identification and characterization of two dermorphins from skin extracts of the Amazonian frog Phyllomedusa bicolor.

A;Reference number: S21152; MUID:92339502; PMID:1633846

A;Accession: S21152

A;Molecule type: protein

A;Residues: 1-13 <MIG>

A;Experimental source: skin

C;Superfamily: unassigned animal peptides

Query Match 24.7%; Score 20; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVLPV 9
|: ||
Db 9 PIYPV 13

RESULT 30

B47415

mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)

N;Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996

C;Accession: B47415

R;Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.

J. Biol. Chem. 268, 17943-17950, 1993

A;Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and utilization to prepare photoaffinity analogs.

A;Reference number: A47415; MUID:93352609; PMID:7688733
A;Accession: B47415
A;Molecule type: protein
A;Residues: 1-13 <SZU>
A;Experimental source: liver
C;Complex: The enzyme appears to be a heterodimer of alpha and beta chains.
C;Function:
A;Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP
A;Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 activity)
C;Keywords: blocked amino end; nucleotidyltransferase

Query Match 24.7%; Score 20; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PFPFV 15
| | |
Db 8 PHPFL 12

RESULT 31

H64008

hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998

C;Accession: H64008

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: H64008

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <TIGR>

A;Cross-references: GB:U32731; GB:L42023; NID:g1573465; PID:g1573478; TIGR:HI0492

Query Match 24.7%; Score 20; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVLPEP 11
| : | : |
Db 6 PKMPPKP 12

RESULT 32

PA0024

protein QA300050 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C;Accession: PA0024

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis.

A;Reference number: PA0001

A;Accession: PA0024

A;Molecule type: protein

A;Residues: 1-15 <KAM>

A;Experimental source: seed

Query Match 24.7%; Score 20; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFP 13

|||

Db 6 PFP 8

RESULT 33

A49761

locustapyrokinin - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 08-Dec-1995

C;Accession: A49761

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.

Gen. Comp. Endocrinol. 81, 97-104, 1991

A;Title: Isolation, primary structure, and synthesis of locustapyrokinin: a myotropic peptide of Locusta migratoria.

A;Reference number: A49761; MUID:91224474; PMID:2026322

A;Accession: A49761

A;Molecule type: protein

A;Residues: 1-16 <SCH>

C;Comment: This neuropeptide stimulates contractions in an isolated cockroach hindgut assay system.

C;Superfamily: pyrokinin

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;16/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 24.7%; Score 20; DB 1; Length 16;

Best Local Similarity 60.0%; Pred. No. 3.3e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PVEPF 12

| :||

Db 8 PQQPF 12

RESULT 34

A60551

leukocyte elastase (EC 3.4.21.37) - dog (fragment)
 C;Species: Canis lupus familiaris (dog)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999
 C;Accession: A60551
 R;Axelsson, L.; Bergenfeldt, M.; Bjoerk, P.; Olsson, R.; Ohlsson, K.
 Scand. J. Clin. Lab. Invest. 50, 35-42, 1990
 A;Title: Release of immunoreactive canine leukocyte elastase normally and in
 endotoxin and pancreatitic shock.
 A;Reference number: A60551; MUID:90193608; PMID:1690443
 A;Accession: A60551
 A;Molecule type: protein
 A;Residues: 1-16 <AXE>
 C;Superfamily: trypsin; trypsin homology
 C;Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 24.7%; Score 20; DB 2; Length 16;
 Best Local Similarity 40.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

Qy 8 PVEP--FPFV 15
 | :| :||:
 Db 6 PAQPHAWPFM 15

RESULT 35

A42576
 steroid receptor complex Hsp56 60K component - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Sep-1998
 C;Accession: A42576
 R;Yem, A.W.; Tomasselli, A.G.; Heinrikson, R.L.; Zurcher-Neely, H.; Ruff, V.A.;
 Johnson, R.A.; Deibel Jr., M.R.
 J. Biol. Chem. 267, 2868-2871, 1992
 A;Title: The Hsp56 component of steroid receptor complexes binds to immobilized
 FK506 and shows homology to FKBP-12 and FKBP-13.
 A;Reference number: A42576; MUID:92147620; PMID:1371107
 A;Accession: A42576
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-18 <YEM>
 A;Experimental source: thymus
 A;Note: sequence extracted from NCBI backbone (NCBIP:80696)
 C;Superfamily: human FK506-binding protein FKBP51; BKBP-type peptidylprolyl
 isomerase homology; tetratricopeptide repeat homology
 C;Keywords: steroid hormone receptor

Query Match 24.7%; Score 20; DB 2; Length 18;
 Best Local Similarity 55.6%; Pred. No. 3.8e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 VLPVEPFPPF 14
 | |||
 Db 9 VFEVELFEF 17

RESULT 36

I52614

u-plasminogen activator receptor precursor - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
 C;Accession: I52614
 R;Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.
 Blood 86, 624-635, 1995
 A;Title: A conserved TATA-less proximal promoter drives basal transcription from the urokinase-type plasminogen activator receptor gene.
 A;Reference number: I52614; MUID:95329719; PMID:7605992
 A;Accession: I52614
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-18 <RES>
 A;Cross-references: GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g4261989
 C;Genetics:
 A;Gene: uPAR
 C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 24.7%; Score 20; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLPV 9
 |:|:
 Db 5 PLLPL 9

RESULT 37

A28027

protein P2 - curled-leaved tobacco (fragment)

C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
 C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
 C;Accession: A28027
 R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
 A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-sequence analysis of proteins electroblotted from two-dimensional gel-separated total extracts.
 A;Reference number: A94167
 A;Accession: A28027
 A;Molecule type: protein
 A;Residues: 1-18 <BAU>
 A;Note: 14-Arg was also found

Query Match 24.7%; Score 20; DB 2; Length 18;
 Best Local Similarity 33.3%; Pred. No. 3.8e+03;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VLPVEP 11
 ::|: |
 Db 8 IVPIAP 13

RESULT 38

A40760

basic fibroblast growth factor, long form - pig (fragment)

C;Species: *Sus scrofa domestica* (domestic pig)
 C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 24-Jun-1993
 C;Accession: A40760
 R;Nice, E.C.; Fabri, L.; Whitehead, R.H.; James, R.; Simpson, R.J.; Burgess, A.W.
 J. Biol. Chem. 266, 14425-14430, 1991
 A;Title: The major colonic cell mitogen extractable from colonic mucosa is an N terminally extended form of basic fibroblast growth factor.
 A;Reference number: A40760; MUID:91317799; PMID:1860849
 A;Accession: A40760
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-18 <NIC>

Query Match 24.7%; Score 20; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MPVLP 8
 :| ||
 Db 14 LPALP 18

RESULT 39

B61218

alpha-gliadin 6Ha - grass (*Haynaldia villosa*) (fragment)

C;Species: *Haynaldia villosa*, *Dasypyrum villosum*
 C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999
 C;Accession: B61218
 R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
 Biochem. Genet. 29, 207-211, 1991
 A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of *Haynaldia villosa* Schur (syn. *Dasypyrum villosum* L.).
 A;Reference number: A61218; MUID:91315394; PMID:1859356
 A;Accession: B61218
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <SHE>
 C;Keywords: seed; storage protein

Query Match 23.5%; Score 19; DB 2; Length 10;
 Best Local Similarity 30.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEP 11
 : :|| :||
 Db 1 VRVPVPQLQP 10

RESULT 40

PQ0231

beta-glucosidase (EC 3.2.1.21) - *Cellvibrio gilvus* (fragment)

C;Species: *Cellvibrio gilvus*
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 07-May-1999
 C;Accession: PQ0231
 R;Kashiwagi, Y.; Iijima, C.; Sasaki, T.; Taniguchi, H.
 Agric. Biol. Chem. 55, 2553-2559, 1991

A;Title: Characterization of a beta-glucosidase encoded by a gene from
Cellvibrio gilvus.

A;Reference number: PQ0231; MUID:92144103; PMID:1368758

A;Accession: PQ0231

A;Molecule type: protein

A;Residues: 1-11 <KAS>

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 23.5%; Score 19; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PVEP 11

| ||

Db 4 PAEP 7

RESULT 41

A05174

tryptophyllin-13 - Rohde's leaf frog

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000

C;Accession: A05174

R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.

Int. J. Pept. Protein Res. 27, 175-182, 1986

A;Reference number: A05174

A;Accession: A05174

A;Molecule type: protein

A;Residues: 1-13 <MON>

C;Superfamily: unassigned animal peptides

C;Keywords: pyroglutamic acid; skin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 23.5%; Score 19; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 EMPVLPVEPFP 13

| | | :|

Db 2 EKPYPWPPIYP 12

RESULT 42

A59387

VCAM-1 5'UTR binding protein - Rana pipiens (fragment)

C;Species: Rana pipiens

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C;Accession: A59387

R;BANERJEE, H.

submitted to the Protein Sequence Database, February 2001

A;Description: Identification and characterization of a novel VCAM-1 5'UTR.

A;Reference number: A59387

A;Accession: A59387

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <BAN>

A;Experimental source: CCL-145

A;Note: VCAM-1 5' untranslated region binding protein with a probable translation inhibitory effect

Query Match 23.5%; Score 19; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVEP 11
:|::|
Db 1 IPLDP 5

RESULT 43

S29207

avenin gamma-4 - oat (fragment)

N;Alternate names: CIP-1; coeliac immunoreactive protein 1

C;Species: Avena sativa (oat)

C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998

C;Accession: S29207

R;Rocher, A.; Colilla, F.; Ortiz, M.L.; Mendez, E.

FEBS Lett. 310, 37-40, 1992

A;Title: Identification of the three major coeliac immunoreactive proteins and one alpha-amylase inhibitor from oat endosperm.

A;Reference number: S29207; MUID:92405739; PMID:1526282

A;Accession: S29207

A;Molecule type: protein

A;Residues: 1-15 <ROC>

A;Experimental source: endosperm

C;Superfamily: gliadin

C;Keywords: prolamin; seed

Query Match 23.5%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EPFP 13
:|:|
Db 6 QPYP 9

RESULT 44

I40665

ilvBN leader peptide - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999

C;Accession: I40665

R;Tarleton, J.; Malakooti, J.; Ely, B.

J. Bacteriol. 176, 3765-3774, 1994

A;Title: Regulation of Caulobacter crescentus ilvBN gene expression.

A;Reference number: I40665; MUID:94266730; PMID:8206855

A;Accession: I40665

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-15 <RES>

A;Cross-references: GB:L25317; NID:g408936; PIDN:AAA23046.1; PID:g408937

C;Genetics:

A;Start codon: GTG

C;Superfamily: unassigned leader peptides

Query Match 23.5%; Score 19; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 4.5e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MPVLPVEPF 12
| | | |
Db 5 MIVLMERPF 13

RESULT 45

PA0026

protein QA300027 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C;Accession: PA0026

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis.

A;Reference number: PA0001

A;Accession: PA0026

A;Molecule type: protein

A;Residues: 1-15 <KAM>

A;Experimental source: leaf

Query Match 23.5%; Score 19; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 4.5e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 VLPVEPF 14
| | | |
Db 1 VLKVYGP 9

RESULT 46

A41436

alpha-macroglobulin - green sea turtle (fragment)

C;Species: Chelonia mydas (green sea turtle)

C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 18-Jun-1993

C;Accession: A41436

R;Osada, T.; Sasaki, T.; Ikai, A.

J. Biochem. 103, 212-217, 1988

A;Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin of the green turtle (Chelonia mydas japonica).

A;Reference number: A41436; MUID:88227890; PMID:2453503

A;Accession: A41436

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <OSA>

Query Match 23.5%; Score 19; DB 2; Length 15;
Best Local Similarity 35.7%; Pred. No. 4.5e+03;
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 14

| | : : | | |
Db 1 DPEPQYMVLVPFLF 14

RESULT 47

C61511

milk band B protein - Australian echidna (fragment)

C;Species: Tachyglossus aculeatus (Australian echidna)

C;Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000

C;Accession: C61511

R;Teahan, C.G.; McKenzie, H.A.; Griffiths, M.

Comp. Biochem. Physiol. B 99, 99-118, 1991

A;Title: Some monotreme milk "whey" and blood proteins.

A;Reference number: A61511; MUID:92070088; PMID:1959333

A;Accession: C61511

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <GRI>

C;Keywords: glycoprotein

Query Match 23.5%; Score 19; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FPF 14

|||

Db 13 FPF 15

RESULT 48

T37075

hypothetical protein SCJ30.08 - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T37075

R;Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.;

Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A;Reference number: Z21621

A;Accession: T37075

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-16 <SAN>

A;Cross-references: EMBL:AL109973; PIDN:CAB53303.1; GSPDB:GN00070;

SCOEDB:SCJ30.08

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SCJ30.08

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MPVLPVEP 11

|||: |

Db 1 MPVIRSMP 8

RESULT 49

A45454

ankyrin-binding glycoprotein ABGP, 186K (N-terminal) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

C;Accession: A45454

R;Davis, J.Q.; McLaughlin, T.; Bennett, V.

J. Cell Biol. 121, 121-133, 1993

A;Title: Ankyrin-binding proteins related to nervous system cell adhesion molecules: candidates to provide transmembrane and intercellular connections in adult brain.

A;Reference number: A45454; MUID:93209979; PMID:8458865

A;Accession: A45454

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-16 <DAV>

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIP:128327)

C;Keywords: glycoprotein

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 4.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LEMPVLP 8

:|:|: |

Db 1 IEIPMDP 7

RESULT 50

JQ2030

hypothetical 1.9K protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus

N;Alternate names: ORF2 mini gene protein

C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999

C;Accession: JQ2030

R;Russell, R.L.Q.; Rohrmann, G.F.

J. Gen. Virol. 74, 1191-1195, 1993

A;Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.

A;Reference number: PQ0633; MUID:93286576; PMID:8389803

A;Accession: JQ2030

A;Molecule type: DNA

A;Residues: 1-17 <RUS>

A;Cross-references: DDBJ:D13375; NID:g222217; PIDN:BAA02640.1; PID:d1003144; PID:g222222

Query Match 23.5%; Score 19; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9

||||

Db 2 VLPV 5

Search completed: July 4, 2004, 04:47:17
Job time : 12.5299 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 29.4403 Seconds
(without alignments)
158.601 Million cell updates/sec

Title: US-09-641-802-5
Perfect score: 81
Sequence: 1 DLEMPVLPVEPFPPFV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	81	100.0	15	14	US-10-281-652-5	Sequence 5, Appli
2	36	44.4	18	14	US-10-281-652-22	Sequence 22, Appl
3	34	42.0	15	14	US-10-281-652-8	Sequence 8, Appli
4	32	39.5	15	12	US-10-103-395-97	Sequence 97, Appl
5	32	39.5	15	12	US-10-103-395-111	Sequence 111, App
6	31	38.3	12	14	US-10-158-596A-10	Sequence 10, Appl
7	31	38.3	12	14	US-10-157-775B-10	Sequence 10, Appl
8	31	38.3	12	14	US-10-254-446A-10	Sequence 10, Appl
9	31	38.3	12	14	US-10-155-883B-10	Sequence 10, Appl
10	31	38.3	12	14	US-10-080-608A-179	Sequence 179, App
11	31	38.3	12	15	US-10-370-685-88	Sequence 88, Appl
12	30	37.0	16	14	US-10-161-791-451	Sequence 451, App
13	30	37.0	17	14	US-10-211-088-97	Sequence 97, Appl
14	30	37.0	18	14	US-10-225-567A-1382	Sequence 1382, Ap
15	29	35.8	9	14	US-10-353-929-171	Sequence 171, App
16	29	35.8	14	14	US-10-185-050-56	Sequence 56, Appl
17	29	35.8	16	14	US-10-161-791-202	Sequence 202, App
18	29	35.8	16	14	US-10-161-791-406	Sequence 406, App
19	28	34.6	9	12	US-10-398-104-34	Sequence 34, Appl
20	28	34.6	10	10	US-09-572-404B-218	Sequence 218, App
21	28	34.6	10	10	US-09-572-404B-220	Sequence 220, App
22	28	34.6	10	10	US-09-572-404B-222	Sequence 222, App
23	28	34.6	10	14	US-10-200-708-513	Sequence 513, App
24	28	34.6	10	14	US-10-200-708-538	Sequence 538, App
25	28	34.6	11	12	US-10-398-104-174	Sequence 174, App
26	28	34.6	12	14	US-10-226-007-1252	Sequence 1252, Ap
27	28	34.6	13	14	US-10-226-007-1253	Sequence 1253, Ap
28	28	34.6	13	14	US-10-226-007-1261	Sequence 1261, Ap
29	28	34.6	13	16	US-10-467-209-21	Sequence 21, Appl
30	28	34.6	13	16	US-10-468-370-75	Sequence 75, Appl
31	28	34.6	14	14	US-10-226-007-1254	Sequence 1254, Ap
32	28	34.6	14	14	US-10-226-007-1262	Sequence 1262, Ap
33	28	34.6	14	14	US-10-226-007-1269	Sequence 1269, Ap
34	28	34.6	15	12	US-10-103-395-120	Sequence 120, App
35	28	34.6	15	14	US-10-226-007-1255	Sequence 1255, Ap
36	28	34.6	15	14	US-10-226-007-1263	Sequence 1263, Ap
37	28	34.6	15	14	US-10-226-007-1270	Sequence 1270, Ap
38	28	34.6	15	14	US-10-226-007-1276	Sequence 1276, Ap
39	28	34.6	15	16	US-10-475-853-11	Sequence 11, Appl
40	28	34.6	16	14	US-10-226-007-1256	Sequence 1256, Ap
41	28	34.6	16	14	US-10-226-007-1264	Sequence 1264, Ap
42	28	34.6	16	14	US-10-226-007-1271	Sequence 1271, Ap
43	28	34.6	16	14	US-10-226-007-1277	Sequence 1277, Ap
44	28	34.6	16	14	US-10-226-007-1282	Sequence 1282, Ap
45	28	34.6	17	14	US-10-226-007-1257	Sequence 1257, Ap
46	28	34.6	17	14	US-10-226-007-1265	Sequence 1265, Ap
47	28	34.6	17	14	US-10-226-007-1272	Sequence 1272, Ap
48	28	34.6	17	14	US-10-226-007-1278	Sequence 1278, Ap
49	28	34.6	17	14	US-10-226-007-1283	Sequence 1283, Ap
50	28	34.6	17	14	US-10-226-007-1287	Sequence 1287, Ap
51	28	34.6	17	14	US-10-161-791-360	Sequence 360, App
52	28	34.6	18	9	US-09-879-957-159	Sequence 159, App
53	28	34.6	18	14	US-10-185-050-103	Sequence 103, App
54	28	34.6	18	14	US-10-226-007-1258	Sequence 1258, Ap
55	28	34.6	18	14	US-10-226-007-1266	Sequence 1266, Ap
56	28	34.6	18	14	US-10-226-007-1273	Sequence 1273, Ap

57	28	34.6	18	14	US-10-226-007-1279	Sequence 1279, Ap
58	28	34.6	18	14	US-10-226-007-1284	Sequence 1284, Ap
59	28	34.6	18	14	US-10-226-007-1288	Sequence 1288, Ap
60	28	34.6	18	14	US-10-226-007-1291	Sequence 1291, Ap
61	28	34.6	18	14	US-10-161-791-317	Sequence 317, App
62	28	34.6	18	14	US-10-029-386-33029	Sequence 33029, A
63	27.5	34.0	10	10	US-09-895-298-138	Sequence 138, App
64	27	33.3	8	9	US-09-954-166-12	Sequence 12, Appl
65	27	33.3	8	9	US-09-761-534A-3	Sequence 3, Appli
66	27	33.3	8	9	US-09-434-965-2	Sequence 2, Appli
67	27	33.3	8	14	US-10-145-396-2	Sequence 2, Appli
68	27	33.3	8	14	US-10-046-801-25	Sequence 25, Appl
69	27	33.3	8	14	US-10-046-801-28	Sequence 28, Appl
70	27	33.3	8	14	US-10-266-463A-46	Sequence 46, Appl
71	27	33.3	8	15	US-10-394-980-338	Sequence 338, App
72	27	33.3	9	8	US-08-344-824-97	Sequence 97, Appl
73	27	33.3	9	9	US-09-954-166-13	Sequence 13, Appl
74	27	33.3	9	9	US-09-954-166-14	Sequence 14, Appl
75	27	33.3	9	9	US-09-434-965-1	Sequence 1, Appli
76	27	33.3	9	10	US-09-854-248-29	Sequence 29, Appl
77	27	33.3	9	14	US-10-015-535-4	Sequence 4, Appli
78	27	33.3	9	14	US-10-094-699-20	Sequence 20, Appl
79	27	33.3	9	14	US-10-266-463A-47	Sequence 47, Appl
80	27	33.3	9	14	US-10-239-313A-467	Sequence 467, App
81	27	33.3	9	15	US-10-117-937-47	Sequence 47, Appl
82	27	33.3	10	8	US-08-854-825-40	Sequence 40, Appl
83	27	33.3	10	8	US-08-344-824-382	Sequence 382, App
84	27	33.3	10	9	US-09-894-018-330	Sequence 330, App
85	27	33.3	10	14	US-10-094-699-21	Sequence 21, Appl
86	27	33.3	10	15	US-10-117-937-48	Sequence 48, Appl
87	27	33.3	10	15	US-10-374-535-16	Sequence 16, Appl
88	27	33.3	11	14	US-10-239-313A-521	Sequence 521, App
89	27	33.3	12	10	US-09-954-385-146	Sequence 146, App
90	27	33.3	12	14	US-10-204-987-2	Sequence 2, Appli
91	27	33.3	13	14	US-10-062-710-34	Sequence 34, Appl
92	27	33.3	13	16	US-10-467-209-22	Sequence 22, Appl
93	27	33.3	13	16	US-10-467-209-23	Sequence 23, Appl
94	27	33.3	13	16	US-10-468-370-76	Sequence 76, Appl
95	27	33.3	13	16	US-10-468-370-77	Sequence 77, Appl
96	27	33.3	13	16	US-10-412-964-38	Sequence 38, Appl
97	27	33.3	14	10	US-09-775-052-11	Sequence 11, Appl
98	27	33.3	14	12	US-10-232-884-15	Sequence 15, Appl
99	27	33.3	14	12	US-10-232-884-25	Sequence 25, Appl
100	27	33.3	14	14	US-10-185-050-203	Sequence 203, App

ALIGNMENTS

RESULT 1

US-10-281-652-5

; Sequence 5, Application US/10281652

; Publication No. US20030091606A1

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-5

Query Match 100.0%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPFPPV 15
| | | | | | | | | | | | | | |
Db 1 DLEMPVLPVEPFPPV 15

RESULT 2

US-10-281-652-22

; Sequence 22, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-22

Query Match 44.4%; Score 36; DB 14; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
:: | ||||
Db 3 EMPFPKYPVEPF 14

RESULT 3

US-10-281-652-8

; Sequence 8, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-8

Query Match 42.0%; Score 34; DB 14; Length 15;
Best Local Similarity 70.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEVPFPPF 14
| | || |||
Db 5 PKLKVEVPFPPF 14

RESULT 4

US-10-103-395-97

; Sequence 97, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; TITLE OF INVENTION: RESTRICTED EPITOPES

; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-97

Query Match 39.5%; Score 32; DB 12; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEFPF 13
| |:|:| |
Db 2 LNFPISPIETVP 13

RESULT 5

US-10-103-395-111
; Sequence 111, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; TITLE OF INVENTION: RESTRICTED EPITOPES
; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-111

Query Match 39.5%; Score 32; DB 12; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEFP 13
| |:|:|
Db 4 LNFPISPIETVP 15

RESULT 6

US-10-158-596A-10
; Sequence 10, Application US/10158596A
; Publication No. US20030068900A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela
; APPLICANT: Flynn, Christine
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLE NUCLEATION, SHAPE AND CRYSTAL PHASE
; FILE REFERENCE: 119927-1052
; CURRENT APPLICATION NUMBER: US/10/158,596A
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/296,013
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide retrieved from phage biopanning
US-10-158-596A-10

Query Match 38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LPVEFP 13
||: |||
Db 5 LPMTFP 11

RESULT 7

US-10-157-775B-10
; Sequence 10, Application US/10157775B
; Publication No. US20030073104A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M.
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: NANOSCALING ORDERING OF HYBRID MATERIALS USING GENETICALLY ENGINEERED
; TITLE OF INVENTION: MESOSCALE VIRUS
; FILE REFERENCE: 119927-1051
; CURRENT APPLICATION NUMBER: US/10/157,775B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/326,583

; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide recognition sequence retrieved from phage
biopanning
US-10-157-775B-10

Query Match 38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LPVEPFP 13
||: |||
Db 5 LPMTFPFP 11

RESULT 8

US-10-254-446A-10

; Sequence 10, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from
phage biopanning
US-10-254-446A-10

Query Match 38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LPVEPFP 13
||: |||
Db 5 LPMTFPFP 11

RESULT 9

US-10-155-883B-10

; Sequence 10, Application US/10155883B
; Publication No. US20030148380A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M.
; TITLE OF INVENTION: MOLECULAR RECOGNITION OF MATERIALS
; FILE REFERENCE: 119927-1049
; CURRENT APPLICATION NUMBER: US/10/155,883B
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/296,013
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide binding sequence retrieved from phage biopanning
US-10-155-883B-10

Query Match 38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LPVEFPF 13
||: |||
Db 5 LPMTFPF 11

RESULT 10

US-10-080-608A-179

; Sequence 179, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Identified from M13 bacteriophage peptide display library.

US-10-080-608A-179

Query Match 38.3%; Score 31; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LPVEPFP 13
||: |||
Db 5 LPMTFPFP 11

RESULT 11

US-10-370-685-88

; Sequence 88, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF.P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: binds to GaAs
US-10-370-685-88

Query Match 38.3%; Score 31; DB 15; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LPVEPFP 13
||: |||
Db 5 LPMTFPFP 11

RESULT 12

US-10-161-791-451

; Sequence 451, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York

; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/161,791
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999
 ; FILING DATE: 16-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 451:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 US-10-161-791-451

Query Match 37.0%; Score 30; DB 14; Length 16;
 Best Local Similarity 57.1%; Pred. No. 8e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLPVEP 11
 |:||::|
 Db 6 PLLPIKP 12

RESULT 13

US-10-211-088-97

; Sequence 97, Application US/10211088
 ; Publication No. US20030104479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bright, Gary R.
 ; APPLICANT: Premkumar, D. David
 ; APPLICANT: Chen, Yih-Tai
 ; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For
 Molecular Binding
 ; FILE REFERENCE: 01-1022-US
 ; CURRENT APPLICATION NUMBER: US/10/211,088
 ; CURRENT FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: 60/309,395
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/341,589
 ; PRIOR FILING DATE: 2001-12-13

; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-97

Query Match 37.0%; Score 30; DB 14; Length 17;
Best Local Similarity 62.5%; Pred. No. 8.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DLEMPVLP 8
|||:|:|
Db 7 DLELPLSP 14

RESULT 14

US-10-225-567A-1382

; Sequence 1382, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1382

; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1382

Query Match 37.0%; Score 30; DB 14; Length 18;
Best Local Similarity 41.7%; Pred. No. 9e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
:| | ||::|
Db 6 NLAKPTLPIKTF 17

RESULT 15

US-10-353-929-171

; Sequence 171, Application US/10353929
; Publication No. US20030175288A1
; GENERAL INFORMATION:

; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Tumor antigen
; FILE REFERENCE: GP01-1024
; CURRENT APPLICATION NUMBER: US/10/353,929
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: JP P2000-231814
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide based on the amino acid sequence of SEQ
ID NO:50
US-10-353-929-171

Query Match 35.8%; Score 29; DB 14; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVEFPF 13
:|::|:|
Db 2 IPIQPWP 8

RESULT 16

US-10-185-050-56

; Sequence 56, Application US/10185050

; Publication No. US20030077577A1

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; Kay, Brian K.

; Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING

SAME

; NUMBER OF SEQUENCES: 233

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/185,050

; FILING DATE: 28-Jun-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/826,516

```

;          FILING DATE: 03-Apr-1997
;    ATTORNEY/AGENT INFORMATION:
;          NAME: MISROCK, S. LESLIE
;          REGISTRATION NUMBER: 18,872
;          REFERENCE/DOCKET NUMBER: 1101-208-999
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 790-9090
;          TELEFAX: (212) 896-8864/9741
;          TELEX: 66141 PENNIE
;    INFORMATION FOR SEQ ID NO: 56:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 14 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: unknown
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-185-050-56

```

```

Query Match          35.8%;  Score 29;  DB 14;  Length 14;
Best Local Similarity 45.5%;  Pred. No. 9.8e+02;
Matches      5;  Conservative      1;  Mismatches      5;  Indels      0;  Gaps      0;

```

```

Qy          3 EMPVLPVEFPF 13
             | | | |:|
Db          1 EYPPYPPPPYP 11

```

RESULT 17

```

US-10-161-791-202
; Sequence 202, Application US/10161791
; Publication No. US20030186863A1
;  GENERAL INFORMATION:
;    APPLICANT:  SPARKS, Andrew B.
;    APPLICANT:  KAY, Brian K.
;    APPLICANT:  THORN, Judith M.
;    APPLICANT:  QUILLIAM, Lawrence A.
;    APPLICANT:  DER, Channing J.
;    APPLICANT:  FOWLKES, Dana M.
;    APPLICANT:  RIDER, James E.
;    TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;    TITLE OF INVENTION:  ISOLATING AND USING SAME
;    NUMBER OF SEQUENCES:  467
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/161,791

```

```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 202:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-202

```

```

Query Match          35.8%; Score 29; DB 14; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches      6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1 DLEMPVLP 8
        | | |||
Db      3 DPERPVLP 10

```

RESULT 18

US-10-161-791-406

```

; Sequence 406, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 406:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-406

```

```

Query Match          35.8%; Score 29; DB 14; Length 16;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches      5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 LEMPVLP 8
        |::|||
Db      4 LKLPVLP 10

```

```

RESULT 19
US-10-398-104-34
; Sequence 34, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

```


; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-34

Query Match 34.6%; Score 28; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PVEPFP 13
| :|||
Db 3 PYDPFP 8

RESULT 20

US-09-572-404B-218
; Sequence 218, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 218
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in Unknown at 11-20 and may interact
with Sequence 217
; OTHER INFORMATION: in this patent.
US-09-572-404B-218

Query Match 34.6%; Score 28; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MPVLPVEP 11
: || | ||
Db 2 LPVTPGEP 9

RESULT 21

US-09-572-404B-220
; Sequence 220, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 220

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in Unknown at 10-19 and may interact
with Sequence 219
; OTHER INFORMATION: in this patent.
US-09-572-404B-220

Query Match 34.6%; Score 28; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MPVLPVEP 11
: || | ||
Db 2 LPVTPGEP 9

RESULT 22

US-09-572-404B-222

; Sequence 222, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 222
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in Unknown at 14-23 and may interact
with Sequence 221
; OTHER INFORMATION: in this patent.
US-09-572-404B-222

Query Match 34.6%; Score 28; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MPVLPVEP 11
: || | ||
Db 2 LPVTPGEP 9

RESULT 23

US-10-200-708-513

; Sequence 513, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001

; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-513

Query Match 34.6%; Score 28; DB 14; Length 10;
Best Local Similarity 44.4%; Pred. No. 9.8e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEFP 13
|: |:| |
Db 2 PISPIETVP 10

RESULT 24

US-10-200-708-538
; Sequence 538, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-538

Query Match 34.6%; Score 28; DB 14; Length 10;
Best Local Similarity 44.4%; Pred. No. 9.8e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEFP 13
|: |:| |
Db 2 PISPIETVP 10

RESULT 25

US-10-398-104-174

; Sequence 174, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-174

Query Match 34.6%; Score 28; DB 12; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PVEFP 13
| :|||
Db 4 PYDFP 9

RESULT 26

US-10-226-007-1252

; Sequence 1252, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883

; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1252
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1252

Query Match 34.6%; Score 28; DB 14; Length 12;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | | :
Db 1 DLDTPDPPPPY 12

RESULT 27

US-10-226-007-1253

; Sequence 1253, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1253
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1253

Query Match 34.6%; Score 28; DB 14; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | | :
Db 1 DLDTPDPPPPY 12

RESULT 28

US-10-226-007-1261

; Sequence 1261, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1261
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1261

Query Match 34.6%; Score 28; DB 14; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 2 DLDTPTDPPPPY 13

RESULT 29

US-10-467-209-21
; Sequence 21, Application US/10467209
; Publication No. US20040076991A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED INTERLEUKIN-1 RECEPTOR
; TITLE OF INVENTION: ANTAGONIST (IL-1RA) WITH REDUCED IMMUNOGENICITY
; FILE REFERENCE: MER-110
; CURRENT APPLICATION NUMBER: US/10/467,209
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 01102573.1
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01170
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope of human leptin
US-10-467-209-21

Query Match 34.6%; Score 28; DB 16; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EMPVLPVEP 11
:: |:|:|
Db 2 KIDVVPIEP 10

RESULT 30

US-10-468-370-75

; Sequence 75, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-75

Query Match 34.6%; Score 28; DB 16; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EMPVLPVEP 11
:: |:|:|
Db 2 KIDVVPIEP 10

RESULT 31

US-10-226-007-1254

; Sequence 1254, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:

```
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1254
; LENGTH: 14
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1254
```

```
Query Match          34.6%; Score 28; DB 14; Length 14;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
Matches      5; Conservative      2; Mismatches      5; Indels      0; Gaps      0;
```

```
Qy      1 DLEMPVLPVEPF 12
        ||: | | |:
Db      1 DLDTPDPPPPY 12
```

RESULT 32

```
US-10-226-007-1262
; Sequence 1262, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1262
; LENGTH: 14
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1262
```

```
Query Match          34.6%; Score 28; DB 14; Length 14;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
Matches      5; Conservative      2; Mismatches      5; Indels      0; Gaps      0;
```

```
Qy      1 DLEMPVLPVEPF 12
        ||: | | |:
Db      2 DLDTPDPPPPY 13
```


RESULT 33

US-10-226-007-1269

; Sequence 1269, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1269
; LENGTH: 14
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1269

Query Match 34.6%; Score 28; DB 14; Length 14;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 3 DLDTPDPPPPY 14

RESULT 34

US-10-103-395-120

; Sequence 120, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; TITLE OF INVENTION: RESTRICTED EPITOPES
; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-120

Query Match 34.6%; Score 28; DB 12; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEVFP 13
|: |:| |
Db 3 PISPIETVP 11

RESULT 35

US-10-226-007-1255

; Sequence 1255, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1255
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1255

Query Match 34.6%; Score 28; DB 14; Length 15;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 1 DLDTPTDPPPPY 12

RESULT 36

US-10-226-007-1263

; Sequence 1263, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1263
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1263

Query Match 34.6%; Score 28; DB 14; Length 15;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 2 DLDTPDTPPPPY 13

RESULT 37

US-10-226-007-1270

; Sequence 1270, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1270
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1270

Query Match 34.6%; Score 28; DB 14; Length 15;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 3 DLDTPDTPPPPY 14

RESULT 38

US-10-226-007-1276

```
; Sequence 1276, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1276
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1276
```

```
Query Match          34.6%; Score 28; DB 14; Length 15;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches      5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      1 DLEMPVLPVEPF 12
        ||: | | |:
Db      4 DLDTPDPPPPY 15
```

RESULT 39

US-10-475-853-11

```
; Sequence 11, Application US/10475853
; Publication No. US20040121442A1
; GENERAL INFORMATION:
; APPLICANT: Chet, Ilan
; APPLICANT: Viterbo, Ada
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES
ENCODING SAME,
; TITLE OF INVENTION: PROMOTERS OF SAME AND USES THEREOF
; FILE REFERENCE: 27049
; CURRENT APPLICATION NUMBER: US/10/475,853
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide derived from chit36
US-10-475-853-11
```

```
Query Match          34.6%; Score 28; DB 16; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches      4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 DLEMPVLPVE 10
|::| || :
Db 4 DMQVPGLPAQ 13

RESULT 40

US-10-226-007-1256

; Sequence 1256, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1256
; LENGTH: 16
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1256

Query Match 34.6%; Score 28; DB 14; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | | :
Db 1 DLDTPTDPPPPY 12

RESULT 41

US-10-226-007-1264

; Sequence 1264, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1264
; LENGTH: 16
; TYPE: PRT

; ORGANISM: human herpesvirus 1
US-10-226-007-1264

Query Match 34.6%; Score 28; DB 14; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 2 DLDTPDTPPPY 13

RESULT 42

US-10-226-007-1271

; Sequence 1271, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1271
; LENGTH: 16
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1271

Query Match 34.6%; Score 28; DB 14; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 3 DLDTPDTPPPY 14

RESULT 43

US-10-226-007-1277

; Sequence 1277, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1277
; LENGTH: 16
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1277

Query Match 34.6%; Score 28; DB 14; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 4 DLDTPDPPPPY 15

RESULT 44

US-10-226-007-1282

; Sequence 1282, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1282
; LENGTH: 16
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1282

Query Match 34.6%; Score 28; DB 14; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 5 DLDTPDPPPPY 16

RESULT 45

US-10-226-007-1257

; Sequence 1257, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1257
; LENGTH: 17
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1257

Query Match 34.6%; Score 28; DB 14; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 1 DLDTPDPPPPY 12

RESULT 46

US-10-226-007-1265

; Sequence 1265, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1265
; LENGTH: 17
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1265

Query Match 34.6%; Score 28; DB 14; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 2 DLDTPDPPPPY 13

RESULT 47

US-10-226-007-1272

; Sequence 1272, Application US/10226007
 ; Publication No. US20030105277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
 ; FILE REFERENCE: 5005.01
 ; CURRENT APPLICATION NUMBER: US/10/226,007
 ; CURRENT FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: US 60/313,883
 ; PRIOR FILING DATE: 2001-08-21
 ; NUMBER OF SEQ ID NOS: 1673
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1272
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: human herpesvirus 1
 US-10-226-007-1272

Query Match 34.6%; Score 28; DB 14; Length 17;
 Best Local Similarity 41.7%; Pred. No. 1.7e+03;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
 ||: | | |:
 Db 3 DLDTPDPPPPY 14

RESULT 48

US-10-226-007-1278

; Sequence 1278, Application US/10226007
 ; Publication No. US20030105277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
 ; FILE REFERENCE: 5005.01
 ; CURRENT APPLICATION NUMBER: US/10/226,007
 ; CURRENT FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: US 60/313,883
 ; PRIOR FILING DATE: 2001-08-21
 ; NUMBER OF SEQ ID NOS: 1673
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1278
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: human herpesvirus 1
 US-10-226-007-1278

Query Match 34.6%; Score 28; DB 14; Length 17;

Best Local Similarity 41.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 4 DLDTPDTPPPY 15

RESULT 49

US-10-226-007-1283

; Sequence 1283, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1283
; LENGTH: 17
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1283

Query Match 34.6%; Score 28; DB 14; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 5 DLDTPDTPPPY 16

RESULT 50

US-10-226-007-1287

; Sequence 1287, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1287
; LENGTH: 17
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1287

Query Match 34.6%; Score 28; DB 14; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPF 12
||: | | |:
Db 6 DLDTPDPPPPY 17

Search completed: July 4, 2004, 05:12:27
Job time : 30.4403 secs

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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:51 ; Search time 25.5224 Seconds
(without alignments)
185.436 Million cell updates/sec

Title: US-09-641-802-5
Perfect score: 81
Sequence: 1 DLEMPVLPVEPFPPFV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5664

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description
<hr/>		

1	27	33.3	18	4	Q9NSF0	Q9nsf0 homo sapien
2	26	32.1	8	6	Q9TRX8	Q9trx8 bos taurus
3	26	32.1	18	2	Q56610	Q56610 vibrio chol
4	25	30.9	9	3	Q9P8E5	Q9p8e5 kluyveromyc
5	25	30.9	12	12	Q83139	Q83139 barley stri
6	24	29.6	8	11	P82598	P82598 rattus norv
7	24	29.6	17	6	Q9TRH5	Q9trh5 bos taurus
8	24	29.6	17	16	Q8X4A4	Q8x4a4 escherichia
9	23	28.4	15	7	Q9TNQ1	Q9tnq1 mus sp. bet
10	23	28.4	17	4	Q9UC43	Q9uc43 homo sapien
11	23	28.4	17	11	Q80X06	Q80x06 mus sp. ahd
12	23	28.4	18	11	Q8CJD4	Q8cjd4 rattus norv
13	22.5	27.8	11	2	Q48933	Q48933 mycobacteri
14	22.5	27.8	16	2	P82597	P82597 bacillus sp
15	22	27.2	9	2	P83157	P83157 anabaena sp
16	22	27.2	10	11	Q9QVJ5	Q9qvj5 rattus sp.
17	22	27.2	10	11	Q9QVJ6	Q9qvj6 rattus sp.
18	22	27.2	12	10	P82441	P82441 nicotiana t
19	22	27.2	14	10	P82326	P82326 pisum sativ
20	22	27.2	14	13	Q07378	Q07378 coturnix co
21	22	27.2	15	2	P83076	P83076 bacillus ce
22	22	27.2	15	4	Q9HCX8	Q9hcx8 homo sapien
23	22	27.2	16	4	O00497	O00497 homo sapien
24	22	27.2	16	6	Q9TQY6	Q9tqy6 oryctolagus
25	22	27.2	16	6	O77489	O77489 tupaia glis
26	22	27.2	16	9	Q38407	Q38407 bacteriopha
27	22	27.2	16	12	Q9WMG6	Q9wmg6 sigma virus
28	22	27.2	17	6	Q9TRU8	Q9tru8 bos taurus
29	22	27.2	18	2	Q9R5B0	Q9r5b0 arthrobacte
30	22	27.2	18	4	Q9UCF9	Q9ucf9 homo sapien
31	22	27.2	18	10	Q41458	Q41458 solanum tub
32	21	25.9	9	4	Q9UMF3	Q9umf3 homo sapien
33	21	25.9	9	5	Q9TWV0	Q9twv0 anthopleura
34	21	25.9	11	5	P82700	P82700 leucophaea
35	21	25.9	14	2	Q9ZB42	Q9zb42 streptococc
36	21	25.9	14	2	O85527	O85527 chlamydia t
37	21	25.9	15	8	Q9T2K8	Q9t2k8 spinacia ol
38	21	25.9	17	4	Q9NY39	Q9ny39 homo sapien
39	21	25.9	17	6	Q9TRY8	Q9try8 sus sp. ins
40	21	25.9	18	4	Q9UCL4	Q9ucl4 homo sapien
41	21	25.9	18	4	Q9BQT0	Q9bqt0 homo sapien
42	20	24.7	8	10	Q8L802	Q8l802 zea mays (m
43	20	24.7	9	10	Q9S8J8	Q9s8j8 oryza sativ
44	20	24.7	10	2	P83154	P83154 anabaena sp
45	20	24.7	10	8	Q8WBR7	Q8wbr7 chaitophoru
46	20	24.7	10	10	P81898	P81898 prunus dulc
47	20	24.7	10	15	Q75595	Q75595 human immun
48	20	24.7	12	8	Q9GI96	Q9gi96 sargassum p
49	20	24.7	13	6	Q865C9	Q865c9 sus scrofa
50	20	24.7	14	2	P83159	P83159 anabaena sp
51	20	24.7	15	2	Q9KIV5	Q9kiv5 anabaena sp
52	20	24.7	16	6	Q9TRD1	Q9trd1 sus scrofa
53	20	24.7	16	13	Q9PRU6	Q9pru6 gallus gall
54	20	24.7	17	4	Q9UCD3	Q9ucd3 homo sapien
55	20	24.7	17	13	Q9PRU7	Q9pru7 gallus gall
56	20	24.7	18	8	O98365	O98365 myosurus mi
57	20	24.7	18	11	P70649	P70649 mus sp. syn

58	20	24.7	18	11	P70650	P70650 mus sp. syn
59	19.5	24.1	12	11	Q8R2F6	Q8r2f6 rattus norv
60	19	23.5	9	6	Q9TRU7	Q9tru7 bos taurus
61	19	23.5	12	10	P82328	P82328 pisum sativ
62	19	23.5	12	13	Q9PSW5	Q9psw5 gallus gall
63	19	23.5	13	13	P82866	P82866 rana pipien
64	19	23.5	14	2	Q8RK22	Q8rk22 pseudomonas
65	19	23.5	15	2	Q9R5Z5	Q9r5z5 streptococc
66	19	23.5	15	2	Q46013	Q46013 caulobacter
67	19	23.5	15	4	Q9UCJ8	Q9ucj8 homo sapien
68	19	23.5	15	4	Q9BXQ0	Q9bxq0 homo sapien
69	19	23.5	15	6	P83497	P83497 ovis aries
70	19	23.5	15	6	Q9TRA6	Q9tra6 bos taurus
71	19	23.5	16	2	Q8KMS4	Q8kms4 escherichia
72	19	23.5	16	11	Q9QVM7	Q9qvm7 rattus sp.
73	19	23.5	17	4	Q9UCP4	Q9ucp4 homo sapien
74	19	23.5	17	7	Q31213	Q31213 mus musculu
75	19	23.5	17	8	Q9XNQ1	Q9xnq1 boophilus m
76	19	23.5	17	12	Q65373	Q65373 orgyia pseu
77	19	23.5	18	2	Q8L2T5	Q8l2t5 neisseria m
78	19	23.5	18	4	Q9UCL5	Q9ucl5 homo sapien
79	19	23.5	18	4	Q16244	Q16244 homo sapien
80	19	23.5	18	6	Q9TRG2	Q9trg2 oryctolagus
81	19	23.5	18	12	Q84129	Q84129 influenzavi
82	19	23.5	18	13	Q801Y9	Q801y9 carassius c
83	19	23.5	18	13	Q801Y8	Q801y8 carassius c
84	19	23.5	18	13	Q7ZSX6	Q7zsx6 carassius c
85	18	22.2	9	2	Q99193	Q99193 pseudomonas
86	18	22.2	9	10	Q9FXL0	Q9fxl0 lilium long
87	18	22.2	9	12	Q88612	Q88612 middelburg
88	18	22.2	10	2	Q9R5T2	Q9r5t2 acetobacter
89	18	22.2	10	2	P83160	P83160 anabaena sp
90	18	22.2	10	11	Q63389	Q63389 rattus norv
91	18	22.2	11	8	Q32704	Q32704 nicotiana t
92	18	22.2	11	11	Q61797	Q61797 mus musculu
93	18	22.2	12	2	Q8KT49	Q8kt49 fischerella
94	18	22.2	12	6	Q8MJQ0	Q8mjQ0 saguinus fu
95	18	22.2	12	6	Q8MJP8	Q8mjp8 callimico g
96	18	22.2	12	6	Q8MJP7	Q8mjp7 callithrix
97	18	22.2	12	6	Q8MJP9	Q8mjp9 leontopithe
98	18	22.2	12	6	Q8MJE3	Q8mje3 saimiri sci
99	18	22.2	12	6	Q8MJQ1	Q8mjQ1 ateles fusc
100	18	22.2	12	6	Q8MJE2	Q8mje2 cebus apell

ALIGNMENTS

RESULT 1

Q9NSF0

ID Q9NSF0 PRELIMINARY; PRT; 18 AA.
AC Q9NSF0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MESP1 (Fragment).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carim L., Estivill X., Escarceller M., Sumoy L.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
 RA Lehrach H., Poustka A., Lundberg J.;
 RT "The European IMAGE consortium for integrated Molecular analysis of
 RT human gene transcripts.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL357535; CAB93427.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 18 AA; 2196 MW; 0ACBE7DA3E2849F0 CRC64;

Query Match 33.3%; Score 27; DB 4; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MPVLPVEFPF 13
 ||: |:| |
 Db 5 MPLSPLEWLP 14

RESULT 2

Q9TRX8

ID Q9TRX8 PRELIMINARY; PRT; 8 AA.
 AC Q9TRX8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Osteopontin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91282766; PubMed=1676261;
 RA Prince C.W., Dickie D., Krumdieck C.L.;
 RT "Osteopontin, a substrate for transglutaminase and factor XIII
 RT activity.";
 RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;

Query Match 32.1%; Score 26; DB 6; Length 8;
 Best Local Similarity 62.5%; Pred. No. 1e+06;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LPVEFPF 14
 |||:| |

Db 1 LPVKPXXF 8

RESULT 3

Q56610

ID Q56610 PRELIMINARY; PRT; 18 AA.
AC Q56610;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE AccA (Fragment).
GN ACCA.
OS *Vibrio cholerae*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; *Vibrio*.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6706;
RX MEDLINE=97074686; PubMed=8917113;
RA Franco A., Peir-En Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
RA Morris J.G.;
RT "Cloning and characterization of dnaE, encoding the catalytic subunit
RT of replicative DNA polymerase III, from *Vibrio cholerae* strain
RT C6706.";
RL Gene 175:281-283(1996).
DR EMBL; U30472; AAC44579.1; -.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2153 MW; 18EBCDAD212842EF CRC64;

Query Match 32.1%; Score 26; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVE 10
| | |:::|
Db 7 DFEKPIVELE 16

RESULT 4

Q9P8E5

ID Q9P8E5 PRELIMINARY; PRT; 9 AA.
AC Q9P8E5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HIS4 protein (Fragment).
GN HIS4.
OS *Kluyveromyces lactis* (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; *Kluyveromyces*.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL-Y1140;
RX MEDLINE=99448382; PubMed=10518937;
RA Lamas-Maceiras M., Esperanza Cerdan E., Freire-Picos M.A.;

RT "Kluyveromyces lacxtis HIS4 transcriptional regulation: similarities
 RT and differences to Saccharomyces cerevisiae HIS4 gene.";
 RL FEBS Lett. 458:72-76(1999).
 DR EMBL; AJ238494; CAB87125.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 30.9%; Score 25; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVLPV 9
 :||:|
 Db 2 LPVVPV 7

RESULT 5

Q83139

ID Q83139 PRELIMINARY; PRT; 12 AA.
 AC Q83139;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE (Strain CV17) genomic RNA-gamma, 5' leader.
 OS Barley stripe mosaic virus (BSMV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.
 OX NCBI_TaxID=12327;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV17;
 RX MEDLINE=91062385; PubMed=2247462;
 RA Petty I.T., Edwards M.C., Jackson A.O.;
 RT "Systemic movement of an RNA plant virus determined by a point
 RT substitution in a 5' leader sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8894-8897(1990).
 DR EMBL; M38633; AAA75527.1; -.
 SQ SEQUENCE 12 AA; 1416 MW; 36A281207BC05047 CRC64;

Query Match 30.9%; Score 25; DB 12; Length 12;
 Best Local Similarity 33.3%; Pred. No. 1.8e+03;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MPVLPVEPF 12
 ||:: :: |
 Db 4 MPIIVDSF 12

RESULT 6

P82598

ID P82598 PRELIMINARY; PRT; 8 AA.
 AC P82598;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE 38kDa non-arginase growth inhibitory factor (NAGIF) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=20198203; PubMed=10731662;
 RA Kim K.-Y., Choi I., Kim S.-S.;
 RT "Purification and characterization of a novel inhibitor of the
 RT proliferation of hepatic stellate cells."
 RL J. Biochem. 127:23-27(2000).
 CC -!- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE
 CC HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE
 CC ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.
 CC -!- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG
 CC PROTEIN.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match 29.6%; Score 24; DB 11; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEPF 12
 ||||:
 Db 3 PVEPW 7

RESULT 7

Q9TRH5

ID Q9TRH5 PRELIMINARY; PRT; 17 AA.
 AC Q9TRH5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Alpha-S1-casein homolog (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93231344; PubMed=1299613;
 RA Neuteboom B., Giuffrida M.G., Conti A.;
 RT "Isolation of a new ligand-carrying casein fragment from bovine
 RT mammary gland microsomes."
 RL FEBS Lett. 305:189-191(1992).
 SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 29.6%; Score 24; DB 6; Length 17;
 Best Local Similarity 71.4%; Pred. No. 3.7e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 VEPFPFV 15
 | ||| |
 Db 2 VAPFPEV 8

RESULT 8

Q8X4A4

ID Q8X4A4 PRELIMINARY; PRT; 17 AA.
 AC Q8X4A4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein z4331.
 GN Z4331.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 DR EMBL; AE005528; AAG58115.1; -.
 DR PIR; G85956; G85956.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 17 AA; 1823 MW; 5A1C41BC7EF69D69 CRC64;

Query Match 29.6%; Score 24; DB 16; Length 17;
 Best Local Similarity 80.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFP 13
 | |||
 Db 4 VSPFP 8

RESULT 9

Q9TNQ1

ID Q9TNQ1 PRELIMINARY; PRT; 15 AA.
 AC Q9TNQ1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Beta 2M- class I-binding PEPTIDE=MAJOR histocompatibility complex
 DE H-2KB-specific molecule POORLY associated with beta 2-microglobulin
 DE (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94240094; PubMed=8183884;

RA Joyce S., Kuzushima K., Kepecs G., Angeletti R.H., Nathenson S.G.;
 RT "Characterization of an incompletely assembled major
 RT histocompatibility class I molecule (H-2Kb) associated with unusually
 RT long peptides: implications for antigen processing and presentation."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

Query Match 28.4%; Score 23; DB 7; Length 15;
 Best Local Similarity 50.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LEMPVLPV 9
 |::||: |
 Db 5 LQLPVVKV 12

RESULT 10

Q9UC43

ID Q9UC43 PRELIMINARY; PRT; 17 AA.
 AC Q9UC43;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Interferon-alpha-induced protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96132854; PubMed=8557639;
 RA Rich S.A., Bose M., Tempst P., Rudofsky U.H.;
 RT "Purification, microsequencing, and immunolocalization of p36, a new
 RT interferon-alpha-induced protein that is associated with human lupus
 RT inclusions."
 RL J. Biol. Chem. 271:1118-1126(1996).
 SQ SEQUENCE 17 AA; 2027 MW; 762BE7300049ACEC CRC64;

Query Match 28.4%; Score 23; DB 4; Length 17;
 Best Local Similarity 83.3%; Pred. No. 5.4e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVLPE 10
 ||| ||
 Db 8 PVLTV 13

RESULT 11

Q80X06

ID Q80X06 PRELIMINARY; PRT; 17 AA.
 AC Q80X06;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Ahd-2 (Fragment).
 GN AHD-2.
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95085815; PubMed=7993664;
 RA Bond S.L., Singh S.M.;
 RT "DNA sequence analysis of the cytosolic acetaldehyde dehydrogenase
 RT gene (Ahd-2) in mouse strains with variable ethanol preferences.";
 RL Biochem. Med. Metab. Biol. 52:155-159(1994).
 DR EMBL; S77047; AAP31992.1; -.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1693 MW; F9C85AF9D2773B5E CRC64;

Query Match 28.4%; Score 23; DB 11; Length 17;
 Best Local Similarity 33.3%; Pred. No. 5.4e+03;
 Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEFP 13
 : | | | |
 Db 1 MSSPAQPAVPAP 12

RESULT 12

Q8CJD4

ID Q8CJD4 PRELIMINARY; PRT; 18 AA.
 AC Q8CJD4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Podocin (Fragment).
 GN NPHS2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morita H., Yoshimura A., Makino R., Inui K., Nakao N., Usami T.,
 RA Roselli S., Antignac C., Matsuyama M., Ideura T.;
 RT "Rat genome fragment containing a part of exons and all of the 3'UTR
 RT of Nphs2 as well as microsatellite sites.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB094124; BAC23094.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 18 AA; 2033 MW; D47829DCFFF0EF4B CRC64;

Query Match 28.4%; Score 23; DB 11; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEP 11
 ||||
 Db 4 PVEP 7

RESULT 13

Q48933

ID Q48933 PRELIMINARY; PRT; 11 AA.
 AC Q48933; P77701; Q48932;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Alkyl hydroperoxide reductase C (Fragment).
 GN AHPC.
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC35728, and ATCC35727;
 RA Zhang Y., Deretic V.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC35735;
 RX MEDLINE=96256622; PubMed=8655566;
 RA Dhandayuthapani S., Zhang Y., Deretic V.;
 RT "Oxidative stress response and its role in sensitivity to isoniazid in
 RT mycobacteria: characterization and inducibility of ahpc by peroxides in
 RT Mycobacterium smegmatis and lack of expression in M. aurum and M.
 RT tuberculosis.";
 RL J. Bacteriol. 178:3641-3649(1996).
 DR EMBL; U58031; AAB00320.1; -.
 DR EMBL; U57979; AAA99830.1; -.
 DR EMBL; U57978; AAA99829.1; -.
 DR EMBL; U57762; AAB00317.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1231 MW; 455099E3A87041A7 CRC64;

Query Match 27.8%; Score 22.5; DB 2; Length 11;
 Best Local Similarity 45.5%; Pred. No. 4.1e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 4 MPVLPV-EPFP 13
 ||:| : : ||
 Db 1 MPLLTIGDQFP 11

RESULT 14

P82597

ID P82597 PRELIMINARY; PRT; 16 AA.
 AC P82597;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Thermostable monoacylglycerol lipase (MGLP) (24 kDa) (EC 3.1.1.23)
 DE (Fragment).
 OS Bacillus sp.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1409;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=H-257;
 RX MEDLINE=20198254; PubMed=10731713;
 RA Imamura S., Kitaura S.;
 RT "Purification and characterization of a monoacylglycerol lipase from
 RT the moderately thermophilic Bacillus sp. H-257.";
 RL J. Biochem. 127:419-425(2000).
 CC -!- FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY
 CC OCCURRING WITH 1-MONOLAUROYLGLYCEROL.
 CC -!- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY
 CC INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.
 CC -!- SUBUNIT: MONOMER.
 CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM
 CC TEMPERATURE IS 75 DEGRESS CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.
 CC -!- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS
 CC OTHER BACTERIAL LIPASES.
 DR GO; GO:0047372; F:acylglycerol lipase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Hydrolase.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;

Query Match 27.8%; Score 22.5; DB 2; Length 16;
 Best Local Similarity 54.5%; Pred. No. 6e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 3 EMPVLP-VEPF 12
 : ||| |||
 Db 3 QYPVLSGAEPF 13

RESULT 15
 P83157

ID P83157 PRELIMINARY; PRT; 9 AA.
 AC P83157;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
 OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (OCT-2001) to Swiss-Prot.
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
 CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
 DR GO; GO:0008382; F:iron superoxide dismutase activity; IEA.

DR GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.
 DR GO; GO:0016954; F:nickel superoxide dismutase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Iron; Metal-binding.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 27.2%; Score 22; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EPFPF 14
 || |:
 Db 5 EPLPY 9

RESULT 16

Q9QVJ5

ID Q9QVJ5 PRELIMINARY; PRT; 10 AA.
 AC Q9QVJ5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Myo-inositol hexakisphosphate phosphohydrolase (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91370007; PubMed=1654110;
 RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
 RT "Purification and characterization of phytase from rat intestinal
 RT mucosa."
 RL Biochim. Biophys. Acta 1075:75-82(1991).
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1096 MW; 37A8EA4B1B1B02D7 CRC64;

Query Match 27.2%; Score 22; DB 11; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4.5e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPVE 10
 |:|||
 Db 1 VIPVE 5

RESULT 17

Q9QVJ6

ID Q9QVJ6 PRELIMINARY; PRT; 10 AA.
 AC Q9QVJ6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE MYO-inositol hexakisphosphate phosphohydrolase (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91370007; PubMed=1654110;
 RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
 RT "Purification and characterization of phytase from rat intestinal
 RT mucosa."
 RL Biochim. Biophys. Acta 1075:75-82(1991).
 SQ SEQUENCE 10 AA; 1124 MW; 28B8EA4B1B1B02D7 CRC64;

Query Match 27.2%; Score 22; DB 11; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4.5e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPVE 10
 | : | | |
 Db 1 VIPVE 5

RESULT 18

P82441

ID P82441 PRELIMINARY; PRT; 12 AA.
 AC P82441;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 26 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture."
 RL Planta 0:0-0(2000).
 CC -!- SUBCELLULAR LOCATION: CELL WALL.
 CC -!- TISSUE SPECIFICITY: XYLEM.
 DR GO:0005618; C:cell wall; IEA.
 KW Cell wall.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1234 MW; 340012240872C9D7 CRC64;

Query Match 27.2%; Score 22; DB 10; Length 12;
 Best Local Similarity 80.0%; Pred. No. 5.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PFPFV 15
 | | | |

Db

3 PAPFV 7

RESULT 19

P82326

ID P82326 PRELIMINARY; PRT; 14 AA.
AC P82326;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of lumenal and peripheral thylakoid proteins."
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009579; C:thylakoid; IEA.
KW Chloroplast; Thylakoid.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;

Query Match 27.2%; Score 22; DB 10; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 MPVLPVEP 11
:| | ||
Db 5 LPPLSTEP 12

RESULT 20

Q07378

ID Q07378 PRELIMINARY; PRT; 14 AA.
AC Q07378;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pairedbox and homeobox (Fragment).
GN PAX-QNR.
OS Coturnix coturnix (Common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.

OX NCBI_TaxID=9091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ssp. japonicus; TISSUE=Spinal cord;
 RX MEDLINE=93264300; PubMed=8098617;
 RA Dozier C., Carriere C., Grevin D.;
 RT "Structure and DNA binding properties of PAX-QNR, a paired Box- and
 RT Homeobox-containing Gene.";
 RL Cell Growth Differ. 4:281-289(1993).
 DR EMBL; X68169; CAA48271.1; -.
 DR PIR; B56884; B56884.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1412 MW; 8EBB4EE821E0B9D5 CRC64;

Query Match 27.2%; Score 22; DB 13; Length 14;
 Best Local Similarity 50.0%; Pred. No. 6.3e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PVLPVEPF 12
 | | | |
 Db 1 PTPVSSF 8

RESULT 21

P83076

ID P83076 PRELIMINARY; PRT; 15 AA.
 AC P83076;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE, AND INDUCTION.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to Swiss-Prot.
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- INDUCTION: BY PH REGULATION.
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
 DR GO; GO:0008382; F:iron superoxide dismutase activity; IEA.
 DR GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.
 DR GO; GO:0016954; F:nickel superoxide dismutase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Iron.

FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1615 MW; 579E9483EA474062 CRC64;

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 6.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EMPVLP 8
|:| ||
Db 4 ELPNLP 9

RESULT 22

Q9HCX8

ID Q9HCX8 PRELIMINARY; PRT; 15 AA.
AC Q9HCX8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE cAMP-specific phosphodiesterase 4D.
GN PDE4DN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20374482; PubMed=10913353;
RA Miro X., Casacuberta J.M., Gutierrez-Lopez M.D., Landazuri M.O.,
RA Puigdomenech P.;
RT "Phosphodiesterases 4D and 7A splice variants in the response of HUVEC
RT cells to TNF-alpha.";
RL Biochem. Biophys. Res. Commun. 274:415-421(2000).
DR EMBL; AJ250852; CAC03756.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; NAS.
DR GO; GO:0009187; P:cyclic nucleotide metabolism; ISS.
SQ SEQUENCE 15 AA; 1972 MW; 36C1CF0521236FEE CRC64;

Query Match 27.2%; Score 22; DB 4; Length 15;
Best Local Similarity 44.4%; Pred. No. 6.8e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VLPVEPFPPF 14
:: | |||
Db 1 MMHVNNFPF 9

RESULT 23

O00497

ID O00497 PRELIMINARY; PRT; 16 AA.
AC O00497;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA mismatch repair protein (Fragment).
GN HMLH1.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Palmirotta R., Veri M.C., Curia M.C., Aceto G., D'Amico F.,
 RA Esposito D.L., Mariani-Costantini R., Messerini L., Mori S., Cama A.,
 RA Battista P.;
 RT "Transcripts with splicings of exons 15 and 16 of the hMLH1 gene in
 RT normal lymphocytes: implications in RNA-based mutation screening of
 RT hereditary nonpolyposis colorectal cancer."
 RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF001359; AAB58936.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 16 AA; 1850 MW; 996602B4FFF583D2 CRC64;

Query Match 27.2%; Score 22; DB 4; Length 16;
 Best Local Similarity 57.1%; Pred. No. 7.3e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LEMPVLP 8
 | :| ||
 Db 10 LTLPCLP 16

RESULT 24

Q9TQY6

ID Q9TQY6 PRELIMINARY; PRT; 16 AA.
 AC Q9TQY6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Annexin I (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96226532; PubMed=8967522;
 RA Mayran N., Traverso V., Maroux S., Massey-Harroche D.;
 RT "Cellular and subcellular localizations of annexins I, IV, and VI in
 RT lung epithelia."
 RL Am. J. Physiol. 270:L863-L871(1996).
 DR HSSP; P19619; 1HM6.
 SQ SEQUENCE 16 AA; 1546 MW; 70AA0A45193C8BB6 CRC64;

Query Match 27.2%; Score 22; DB 6; Length 16;
 Best Local Similarity 44.4%; Pred. No. 7.3e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PVLPEPFP 13
 | | :|
 Db 4 PGSAVSPYP 12

RESULT 25

O77489

ID O77489 PRELIMINARY; PRT; 16 AA.
AC O77489;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE D4 dopamine receptor (D4DR) (Fragment).
OS Tupaia glis (Tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaia.
OX NCBI_TaxID=9395;
RN [1]
RP SEQUENCE FROM N.A.
RA Inoue-Murayama M., Takenaka O., Murayama Y.;
RT "Origin and divergence of tandem repeats of primate D4 dopamine
RT receptor genes."
RL Primates 39:217-224(1998).
DR EMBL; AB016198; BAA32036.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1577 MW; 3865AEE77FB63E09 CRC64;

Query Match 27.2%; Score 22; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEVPF 12
| | :||
Db 3 PGSPQDPF 10

RESULT 26

Q38407

ID Q38407 PRELIMINARY; PRT; 16 AA.
AC Q38407;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Bacteriophage miniplasmid P1 parB (Fragment).
OS Bacteriophage P1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P1-like viruses.
OX NCBI_TaxID=10678;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85251477; PubMed=2990410;
RA Austin S., Abeles A.L.;
RT "The partition functions of P1, P7, and F miniplasmids."
RL Basic Life Sci. 30:215-226(1985).
DR EMBL; M36425; AAA32420.1; -.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1938 MW; E938D35BE55088DC CRC64;

Query Match 27.2%; Score 22; DB 9; Length 16;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LPVEPFPPF 14
| : || |
Db 7 LKLSPFKF 14

RESULT 27

Q9WMG6

ID Q9WMG6 PRELIMINARY; PRT; 16 AA.
AC Q9WMG6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE 2 protein (Fragment).
GN 2.
OS Sigma virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OX NCBI_TaxID=11301;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212481; PubMed=8384742;
RA Teninges D., Bras F., Dezelee S.;
RT "Genome organization of the sigma rhabdovirus: six genes and a gene
RT overlap.";
RL Virology 193:1018-1023(1993).
DR EMBL; S57847; AAD40699.1; -.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1904 MW; F96DBC468601967E CRC64;

Query Match 27.2%; Score 22; DB 12; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.3e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVLP 8
||||
Db 11 PVLP 14

RESULT 28

Q9TRU8

ID Q9TRU8 PRELIMINARY; PRT; 17 AA.
AC Q9TRU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Leukemia inhibitory factor, LIF=INHIBITOR of aortic endothelial cell
DE growth (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92115728; PubMed=1370585;

RA Ferrara N., Winer J., Henzel W.J.;
 RT "Pituitary follicular cells secrete an inhibitor of aortic endothelial
 RT cell growth: identification as leukemia inhibitory factor."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702(1992).
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 27.2%; Score 22; DB 6; Length 17;
 Best Local Similarity 50.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MPVLPV 9
 :|: ||
 Db 3 LPITPV 8

RESULT 29

Q9R5B0

ID Q9R5B0 PRELIMINARY; PRT; 18 AA.
 AC Q9R5B0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE QUINALDINE oxidoreductase beta-subunit (Fragment).
 OS Arthrobacter.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Micrococcaceae.
 OX NCBI_TaxID=1663;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93228843; PubMed=8471177;
 RA de Beyer A., Lingens F.;
 RT "Microbial metabolism of quinoline and related compounds. XVI.
 RT Quinaldine oxidoreductase from Arthrobacter spec. Ru 61a: a molybdenum-
 RT containing enzyme catalysing the hydroxylation at C-4 of the
 RT heterocycle."
 RL Biol. Chem. Hoppe-Seyler 374:101-109(1993).
 SQ SEQUENCE 18 AA; 2043 MW; DF19848087DE5EE1 CRC64;

Query Match 27.2%; Score 22; DB 2; Length 18;
 Best Local Similarity 42.9%; Pred. No. 8.2e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 VEPFPFV 15
 : || |:
 Db 2 MHPFQFI 8

RESULT 30

Q9UCF9

ID Q9UCF9 PRELIMINARY; PRT; 18 AA.
 AC Q9UCF9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C1-INHIBITOR=SERINE proteinase inhibitor (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93264944; PubMed=8495195;
 RA Aulak K.S., Davis A.E.III., Donaldson V.H., Harrison R.A.;
 RT "Chymotrypsin inhibitory activity of normal C1-inhibitor and a P1 Arg
 RT to His mutant: evidence for the presence of overlapping reactive
 RT centers.";
 RL Protein Sci. 2:727-732(1993).
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; 1.
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2120 MW; 6A614E7BF9F54A85 CRC64;

Query Match 27.2%; Score 22; DB 4; Length 18;
 Best Local Similarity 66.7%; Pred. No. 8.2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EPFPFV 15
 :|| ||
 Db 12 QPFLFV 17

RESULT 31

Q41458

ID Q41458 PRELIMINARY; PRT; 18 AA.
 AC Q41458;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE HMG-CoA reductase (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kennebec; TISSUE=Anther;
 RX MEDLINE=95306778; PubMed=7787174;
 RA Bhattacharyya M.K., Paiva N.L., Dixon R.A., Korth K.L., Stermer B.A.;
 RT "Features of the hmg 1 subfamily of genes encoding HMG-CoA reductase
 RT in potato.";
 RL Plant Mol. Biol. 28:1-15(1995).
 DR EMBL; L34830; AAC37437.1; -.
 DR PIR; S56715; S56715.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2181 MW; FD17C510527AA68F CRC64;

Query Match 27.2%; Score 22; DB 10; Length 18;
 Best Local Similarity 57.1%; Pred. No. 8.2e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVLPEP 11
 || |:
 Db 7 PVKPLYP 13

RESULT 32

Q9UMF3

ID Q9UMF3 PRELIMINARY; PRT; 9 AA.
 AC Q9UMF3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PD-1 protein (Fragment).
 GN PD-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97473511; PubMed=9332365;
 RA Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
 RA Burrows P.D., Billips L.G.;
 RT "The human PD-1 gene: complete cDNA, genomic organization, and
 RT developmentally regulated expression in B cell progenitors."
 RL Gene 197:177-187(1997).
 DR EMBL; U64864; AAC51774.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1067 MW; DD4A676DC6C76046 CRC64;

Query Match 25.9%; Score 21; DB 4; Length 9;
 Best Local Similarity 42.9%; Pred. No. 1e+06;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LPVEPFP 13
 :| |:
 Db 3 IPQAPWP 9

RESULT 33

Q9TWV0

ID Q9TWV0 PRELIMINARY; PRT; 9 AA.
 AC Q9TWV0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Antho-RPAMIDE=NEUROPEPTIDE.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynantheae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93126143; PubMed=1480510;
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;

RT "Isolation of Leu-Pro-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
RT an N-terminally protected, biologically active neuropeptide from sea
RT anemones.";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 25.9%; Score 21; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LPVEFPF 13
|| ||
Db 1 LPPGPLP 7

RESULT 34

P82700

ID P82700 PRELIMINARY; PRT; 11 AA.
AC P82700;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Periviscerokinin-3 (LEM-PVK-3).
OS Leucophaea maderae (Madeira cockroach),
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS Blaberus craniifer,
OS Blaptica dubia (Argentinian wood cockroach), and
OS Gromphadorina portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinins from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 25.9%; Score 21; DB 5; Length 11;
Best Local Similarity 80.0%; Pred. No. 7.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PFPFV 15
||| |
Db 7 PFPRV 11

RESULT 35

Q9ZB42

ID Q9ZB42 PRELIMINARY; PRT; 14 AA.
 AC Q9ZB42;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE SsbA (Fragment).
 GN SSBA.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS101;
 RA Podbielski A., Woischnik M., Leonard B.A.B., Schmidt K.H.;
 RT "Characterization of nra, a global negative regulator gene in group A
 RT streptococci."
 RL Mol. Microbiol. 31:0-0(1999).
 DR EMBL; U49397; AAC97153.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1618 MW; 47074F277A834F17 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 9.2e+03;
 Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DLEMPVLPVEPFPPF 14
 || || : ||
 Db 1 DLVDLVLEEDTLPPF 14

RESULT 36

O85527

ID O85527 PRELIMINARY; PRT; 14 AA.
 AC O85527;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Major outer membrane protein (Fragment).
 GN OMP-1.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B3a;
 RA Hsieh Y.-H., Bobo L.D.;
 RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
 RT trachomatis in trachoma endemic villages, Kongwa, Tanzania."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF070289; AAC25259.1; -.
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1399 MW; 39D7E3FF813466B7 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVEP 11
|:|
Db 3 LPLDP 7

RESULT 37

Q9T2K8

ID Q9T2K8 PRELIMINARY; PRT; 15 AA.
AC Q9T2K8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE LHCII kinase, 64 kDa kinase (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=92183823; PubMed=1544419;
RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;
RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with
the cytochrome complex.";
RL FEBS Lett. 298:33-35(1992).
DR PIR; S20410; S20410.
DR PIR; S66419; S66419.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;

Query Match 25.9%; Score 21; DB 8; Length 15;
Best Local Similarity 75.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PVL P 8
|:|
Db 2 PILP 5

RESULT 38

Q9NY39

ID Q9NY39 PRELIMINARY; PRT; 17 AA.
AC Q9NY39;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHI3L1 protein (Fragment).
GN CHI3L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ammon C., Rehli M., Andreesen R., Krause S.W.;
 RT "Alternative splicing of the human cartilage gp-39 gene generates
 RT multiple mRNA transcripts encoding for at least four putative protein
 RT isoforms with distinct carboxyl termini."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ251847; CAB76474.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 17 AA; 2099 MW; 086B9AA863393785 CRC64;

Query Match 25.9%; Score 21; DB 4; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LEMPVLPV 9
 | :| ||:
 Db 9 LFIPTLPL 16

RESULT 39

Q9TRY8

ID Q9TRY8 PRELIMINARY; PRT; 17 AA.
 AC Q9TRY8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Insulin-like growth factor-binding protein-3, IGFBP-3 (Fragment).
 OS Sus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9826;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92049376; PubMed=1719383;
 RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
 RT "Isolation and molecular cloning of insulin-like growth factor-binding
 RT protein-6."
 RL Mol. Endocrinol. 5:938-948(1991).
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1618 MW; 14B17C38D32A400F CRC64;

Query Match 25.9%; Score 21; DB 6; Length 17;
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVLPEP 11
 ||: ||
 Db 9 PVVRXEP 15

RESULT 40

Q9UCL4

ID Q9UCL4 PRELIMINARY; PRT; 18 AA.

AC Q9UCL4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Insulin-like growth factor binding protein 30 kDa form (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93091816; PubMed=1726837;
 RA Roghani M., Segovia B., Whitechurch O., Binoux M.;
 RT "Purification from human cerebrospinal fluid of insulin-like growth
 RT factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered form
 RT of IGFBP-3 and a new IGFBP species."
 RL Growth Regul. 1:125-130(1991).
 SQ SEQUENCE 18 AA; 1689 MW; 10F5516240C6298B CRC64;

Query Match 25.9%; Score 21; DB 4; Length 18;
 Best Local Similarity 57.1%; Pred. No. 1.2e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVLPVEP 11
 ||: ||
 Db 9 PVVRXEP 15

RESULT 41

Q9BQT0

ID Q9BQT0 PRELIMINARY; PRT; 18 AA.
 AC Q9BQT0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21195339; PubMed=11297743;
 RA Holzmann K., Ambrosch I., Elbling L., Micksche M., Berger W.;
 RT "A small upstream open reading frame causes inhibition of human major
 RT vault protein expression from a ubiquitous mRNA splice variant."
 RL FEBS Lett. 494:99-104(2001).
 DR EMBL; AJ291367; CAC35315.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11CB828 CRC64;

Query Match 25.9%; Score 21; DB 4; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1.2e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MPVLPV 9
 :| |||

RESULT 42

Q8L802

ID Q8L802 PRELIMINARY; PRT; 8 AA.
 AC Q8L802;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Pat (Fragment).
 GN PAT.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ronning S.B., Berdal K.G., Vaitilingom M.M., Holst-Jensen A.;
 RT "Transformation event-specific quantitative real-time PCR for
 RT genetically modified Bt11 maize (Zea mays) and estimation of the
 RT impact of exogenous DNA on the limit of quantification."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY123624; AAM89275.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 909 MW; 6046C1B2D77412D7 CRC64;

Query Match 24.7%; Score 20; DB 10; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVLPV 9
 || ||
 Db 1 PVRPV 5

RESULT 43

Q9S8J8

ID Q9S8J8 PRELIMINARY; PRT; 9 AA.
 AC Q9S8J8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORYZATENSIN=BIOACTIVE peptide.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95102521; PubMed=7804141;
 RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
 RT "Isolation and characterization of oryzatensin: a novel bioactive
 RT peptide with ileum-contracting and immunomodulating activities derived
 RT from rice albumin.";

RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR Gramene; Q9S8J8; -.
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 24.7%; Score 20; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PVEFPF 13
|: | |
Db 3 PMYPLP 8

RESULT 44

P83154

ID P83154 PRELIMINARY; PRT; 10 AA.
AC P83154;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phycobilisome rod-core linker polypeptide cpcG3 (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to Swiss-Prot.
CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISK-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -!- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -!- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.
CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030089; C:phycobilisome; IEA.
DR GO; GO:0009579; C:thylakoid; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
KW Phycobilisome; Photosynthesis; Thylakoid; Membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; 2F9B662B5B172737 CRC64;

Query Match 24.7%; Score 20; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 9.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MPVLPVEP 11
:|:| :|
Db 2 LPLLEYKP 9

RESULT 45

Q8WBR7

ID Q8WBR7 PRELIMINARY; PRT; 10 AA.
AC Q8WBR7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN COI.
OS Chaitophorus leucomelas.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Drepanosiphidae; Chaitophorus.
OX NCBI_TaxID=136351;
RN [1]
RP SEQUENCE FROM N.A.
RA Shingleton A.W., Stern D.L.;
RT "Molecular phylogenetic evidence for multiple origins of ant mutualism
RT within the aphid genus Chaitophorus."
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF444288; AAL38565.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;

Query Match 24.7%; Score 20; DB 8; Length 10;
Best Local Similarity 60.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EMPVL 7
|:|:
Db 3 ELPVI 7

RESULT 46

P81898

ID P81898 PRELIMINARY; PRT; 10 AA.
AC P81898;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, small
DE chain (Subunit B) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
DE glycosidase) (N-glycanase) (Fragment).
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RX PubMed=9523720;
RA Altmann F., Paschinger K., Dalik T., Vorauer K.;
RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
RT amidase A and its N-glycans.";

RL Eur. J. Biochem. 252:118-123(1998).
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
 CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
 CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
 CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
 CC CONTAINING AN ASPARTIC RESIDUE.
 CC -!- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
 CC -!- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
 CC DEGLYCOSYLATION.
 CC -!- MASS SPECTROMETRY: MW=21247; METHOD=MALDI.
 DR PIR; B59272; B59272.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0000224; F:peptide-N4-(N-acetyl-beta-glucosaminyl)aspa. . .; IEA.
 KW Hydrolase; Glycoprotein.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1149 MW; 863278CAA1E73771 CRC64;

Query Match 24.7%; Score 20; DB 10; Length 10;
 Best Local Similarity 50.0%; Pred. No. 9.4e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PVEFP 13
 | : ||
 Db 4 PLHDFP 9

RESULT 47

Q75595

ID Q75595 PRELIMINARY; PRT; 10 AA.
 AC Q75595;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Tat protein (Fragment).
 GN TAT.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=T12B;
 RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
 RT "The TAT and C2-V3 Envelope Genes in the Molecular Epidemiology of
 RT Human Immunodeficiency Virus-1."
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U57303; AAB17863.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1182 MW; 22252E34176AB2D7 CRC64;

Query Match 24.7%; Score 20; DB 15; Length 10;
 Best Local Similarity 75.0%; Pred. No. 9.4e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVEP 11
 ||:|
 Db 3 PVDP 6

RESULT 48

Q9GI96

ID Q9GI96 PRELIMINARY; PRT; 12 AA.
AC Q9GI96;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (Fragment).
GN RBCS.
OS Sargassum polycystum.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OX NCBI_TaxID=127578;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=nep127;
RA Phillips N.E.;
RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
RT (Fucales, Phaeophyceae).";
RL Thesis (1998), University of Hawaii.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=nep127;
RA Phillips N.E., Smith C.M., Morden C.W.;
RT "Testing the systematics of the genus Sargassum (Fucales,
RT Phaeophyceae) with the Rubisco operon."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244344; AAF98114.1; -.
DR GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1379 MW; 373D121250CEB867 CRC64;

Query Match 24.7%; Score 20; DB 8; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FPFV 15
| | |:
Db 8 FPFL 11

RESULT 49

Q865C9

ID Q865C9 PRELIMINARY; PRT; 13 AA.
AC Q865C9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutamine synthetase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim J.G., Vallet J.L., Christenson R.K.;
 RT "Characterization of porcine glutamine synthetase."
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY216477; AAO64254.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1555 MW; 87987A0B71AB6B1A CRC64;

Query Match 24.7%; Score 20; DB 6; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EPFPF 14
 ||| :
 Db 7 EPFQY 11

RESULT 50

P83159

ID P83159 PRELIMINARY; PRT; 14 AA.
 AC P83159;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated,
 DE rod (Fragment).
 OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (OCT-2001) to Swiss-Prot.
 CC -!- FUNCTION: ROD LINKER PROTEIN, ASSOCIATED WITH PHYCOCYANIN. LINKER
 CC POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION
 CC OF THE DISK-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME
 CC AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A
 CC DIRECTED AND OPTIMAL ENERGY TRANSFER.
 CC -!- SUBCELLULAR LOCATION: THIS PROTEIN OCCURS IN THE ROD, IT IS
 CC ASSOCIATED WITH PHYCOCYANIN (BY SIMILARITY).
 CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
 DR GO; GO:0030089; C:phycobilisome; IEA.
 DR GO; GO:0015979; P:photosynthesis; IEA.
 KW Phycobilisome; Photosynthesis.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1405 MW; 96823E44F60A3115 CRC64;

Query Match 24.7%; Score 20; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1.3e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LPVEPF 12
 | |||
 Db 9 LGTEPF 14

Search completed: July 4, 2004, 04:45:35
Job time : 27.5224 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 5.14925 Seconds
(without alignments)
151.683 Million cell updates/sec

Title: US-09-641-802-5
Perfect score: 81
Sequence: 1 DLEMPVLPVEPFPPFV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8						
		Query						
Result	No.	Score	Match	Length	DB	ID	Description	
1	25	30.9	15	1	UC17	MAIZE	P80623	zea mays (m
2	23	28.4	12	1	TM2A	METMA	P80652	methanosarc
3	23	28.4	15	1	SODM	ENTAE	P22799	enterobacte
4	22.5	27.8	17	1	RM35	YEAST	P36530	saccharomyc
5	21	25.9	10	1	FAR6	PANRE	P82660	panagrellus
6	21	25.9	13	1	YPE2	LACLC	P42021	lactococcus
7	21	25.9	15	1	UC25	MAIZE	P80631	zea mays (m
8	21	25.9	15	1	UC30	MAIZE	P80636	zea mays (m
9	21	25.9	17	1	A45K	MYCBO	P80069	mycobacteri
10	20	24.7	7	1	ALL3	CARMA	P81806	carcinus ma
11	20	24.7	14	1	ECDC	LYMDI	P80940	lymantria d
12	20	24.7	15	1	SODM	STRGR	P80733	streptomyce
13	20	24.7	16	1	LPK1	LOCMI	P20404	locusta mig
14	19	23.5	10	1	RT02	BOVIN	P82923	bos taurus
15	19	23.5	11	1	CSI5	BACSU	P81095	bacillus su
16	19	23.5	13	1	TY13	PHYRO	P04096	phyllomedus
17	19	23.5	15	1	UC08	MAIZE	P80614	zea mays (m

18	18.5	22.8	15	1	GLN2_PINPS	P81107	pinus pinas
19	18.5	22.8	15	1	UC29_MAIZE	P80635	zea mays (m
20	18	22.2	9	1	UPA3_HUMAN	P30089	homo sapien
21	18	22.2	11	1	EFG_CLOPA	P81350	clostridium
22	18	22.2	13	1	FIBB_RABIT	P14478	oryctolagus
23	18	22.2	13	1	PEDI_HYDAT	P80578	hydra atten
24	18	22.2	13	1	SODM_CANFA	P54712	canis famil
25	18	22.2	13	1	TEME_RANTE	P56920	rana tempor
26	18	22.2	14	1	ATP6_SPIOL	P80086	spinacia ol
27	18	22.2	14	1	UC15_MAIZE	P80621	zea mays (m
28	18	22.2	16	1	AF1S_MALPA	P83140	malva parvi
29	18	22.2	17	1	GPX4_PINPS	P81087	pinus pinas
30	18	22.2	18	1	HEMH_THETS	P80155	theromyzon
31	17	21.0	7	1	ALL4_CARMA	P81807	carcinus ma
32	17	21.0	7	1	CARP_MYTED	P10420	mytilus edu
33	17	21.0	9	1	AL10_CARMA	P81813	carcinus ma
34	17	21.0	9	1	LMT3_LOCFI	P41489	locusta mig
35	17	21.0	10	1	ANG1_BOTJA	Q10581	bothrops ja
36	17	21.0	10	1	ANGT_BOVIN	P01017	bos taurus
37	17	21.0	10	1	ANGT_CHICK	P01018	gallus gall
38	17	21.0	11	1	ANGT_CRIGE	P09037	crinia geor
39	17	21.0	11	1	BPP_AGKHP	P04562	agkistrodon
40	17	21.0	13	1	MP1_MICOC	P81532	microplitis
41	17	21.0	15	1	CBPB_PROAT	P19628	protopterus
42	17	21.0	15	1	SAL1_ONCFI	P81369	oncorhynch
43	17	21.0	15	1	UBL1_MONDO	P50103	monodelphis
44	17	21.0	16	1	FOR2_MYRGU	P81437	myrmecia gu
45	17	21.0	17	1	PSBL_SYNVU	P12241	synechococc
46	17	21.0	18	1	ALL2_CYDPO	P82153	cydia pomon
47	16	19.8	8	1	ANG2_BOTJA	Q10582	bothrops ja
48	16	19.8	9	1	UPA7_HUMAN	P30093	homo sapien
49	16	19.8	10	1	TMOF_AEDAE	P19425	aedes aegyp
50	16	19.8	10	1	UHA3_HUMAN	P40930	homo sapien
51	16	19.8	11	1	BPPB_AGKHA	P01021	agkistrodon
52	16	19.8	11	1	CX5A_CONAL	P58848	conus aulic
53	16	19.8	12	1	TKN1_KASMA	P08613	kassina mac
54	16	19.8	13	1	BLAC_STRGR	P81173	streptomyce
55	16	19.8	13	1	CRBL_VESTR	P17231	vespa tropi
56	16	19.8	13	1	ECDE_LYMDI	P80941	lymantria d
57	16	19.8	13	1	LMT4_LOCFI	P41490	locusta mig
58	16	19.8	13	1	TEMC_RANTE	P56918	rana tempor
59	16	19.8	13	1	UHA3_CANFA	P56535	canis famil
60	16	19.8	14	1	ANGT_HORSE	P01016	equus cabal
61	16	19.8	14	1	CAL1_CALGI	P20728	calotropis
62	16	19.8	15	1	MK2A_PALPR	P80409	palomena pr
63	16	19.8	15	1	UC16_MAIZE	P80622	zea mays (m
64	16	19.8	16	1	MK2B_PALPR	P80410	palomena pr
65	16	19.8	16	1	MK3_PALPR	P80411	palomena pr
66	16	19.8	17	1	APID_BOMPA	P81464	bombus pasc
67	16	19.8	17	1	CHXI_ASPFL	P83488	aspergillus
68	16	19.8	18	1	PA55_SHEEP	P83202	ovis aries
69	15	18.5	7	1	ALL5_CARMA	P81808	carcinus ma
70	15	18.5	7	1	FAR1_HELTI	P41871	helisoma tr
71	15	18.5	8	1	AL15_CARMA	P81818	carcinus ma
72	15	18.5	8	1	ALL3_CYDPO	P82154	cydia pomon
73	15	18.5	8	1	ALL4_CALVO	P41840	calliphora
74	15	18.5	8	1	ALL4_CYDPO	P82155	cydia pomon

75	15	18.5	8	1	ALL5_CALVO	P41841	calliphora
76	15	18.5	8	1	ALL7_CARMA	P81809	carcinus ma
77	15	18.5	8	1	ALL8_CARMA	P81811	carcinus ma
78	15	18.5	8	1	ALL9_CARMA	P81812	carcinus ma
79	15	18.5	8	1	PPK3_PERAM	P82618	periplaneta
80	15	18.5	9	1	MGMT_BOVIN	P29177	bos taurus
81	15	18.5	9	1	ULAH_HUMAN	P31934	homo sapien
82	15	18.5	10	1	AL19_CARMA	P81822	carcinus ma
83	15	18.5	10	1	UPA8_HUMAN	P30094	homo sapien
84	15	18.5	10	1	UXB1_YEAST	P99012	saccharomyc
85	15	18.5	11	1	RR2_CONAM	P42341	conopholis
86	15	18.5	11	1	RRPL_CHAV	P13179	chandipura
87	15	18.5	11	1	TKN1_PSEGU	P42986	pseudophryn
88	15	18.5	11	1	TKN3_PSEGU	P42988	pseudophryn
89	15	18.5	12	1	TKN2_KASMA	P08614	kassina mac
90	15	18.5	13	1	GER1_HORVU	P28525	hordeum vul
91	15	18.5	13	1	GER2_HORVU	P28526	hordeum vul
92	15	18.5	13	1	TEJA_RANJA	P83307	rana japoni
93	15	18.5	13	1	TEMD_RANTE	P56919	rana tempor
94	15	18.5	13	1	UP51_UPEIN	P82036	uperoleia i
95	15	18.5	13	1	VG16_BACSU	P80867	bacillus su
96	15	18.5	14	1	LPER_BACLI	Q04303	bacillus li
97	15	18.5	14	1	MARI_ALTSP	P29399	alteromonas
98	15	18.5	15	1	CKX_WHEAT	P58763	triticum ae
99	15	18.5	15	1	HS11_PINPS	P81083	pinus pinas
100	15	18.5	15	1	LPF_ECOLI	P03057	escherichia

ALIGNMENTS

RESULT 1

UC17_MAIZE

ID UC17_MAIZE STANDARD; PRT; 15 AA.
 AC P80623;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 32)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 42.7 kDa.
 DR Maize-2DPAGE; P80623; COLEOPTILE.
 DR MaizeDB; 123949; -.

FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1554 MW; C0AFF15FFEC8 CRC64;

Query Match 30.9%; Score 25; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LEMPVLPVEP 11
| :|| | |
Db 2 LSPVPFAVAP 11

RESULT 2

TM2A_METMA

ID TM2A_METMA STANDARD; PRT; 12 AA.
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M
DE methyltransferase 28 kDa subunit) (Fragment).
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE.
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=96370840; PubMed=8774736;
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT coenzyme M methyltransferase from Methanosarcina mazei Go1
RT reconstituted in ether lipid liposomes."
RL Eur. J. Biochem. 239:857-864(1996).
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC TETRAHYDROMETHANOPTERIN.
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 28.4%; Score 23; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PVLVP 9
||||:
Db 6 PVLPL 10

RESULT 3

SODM_ENTAE

ID SODM_ENTAE STANDARD; PRT; 15 AA.
AC P22799;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
GN SODA.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE.
RX MEDLINE=91248479; PubMed=1368658;
RA Kim S.W., Lee S.O., Lee T.H.;
RT "Purification and characterization of superoxide dismutase from
RT Aerobacter aerogenes.";
RL Agric. Biol. Chem. 55:101-108(1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR PIR; P0615; P0615.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Metal-binding; Iron.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1756 MW; 352F3D949202E642 CRC64;

Query Match 28.4%; Score 23; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EMPVLP 8
|:| ||
Db 3 ELPQLP 8

RESULT 4

RM35_YEAST

ID RM35_YEAST STANDARD; PRT; 17 AA.
AC P36530;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L35 (YmL35) (Fragment).
GN MRPL35.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91285106; PubMed=2060626;
 RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 RT subunit from yeast mitochondria."
 RL FEBS Lett. 284:51-56(1991).
 DR PIR; S17274; S17274.
 DR GermOnline; 140814; -.
 DR SGD; S0002730; MRPL35.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1826 MW; 6CE89CB415483EE8 CRC64;

Query Match 27.8%; Score 22.5; DB 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 9.4e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 7 LPVEP-FPFV 15
 || :| :| |
 Db 8 LPTDPVYPXV 17

RESULT 5

FAR6_PANRE

ID FAR6_PANRE STANDARD; PRT; 10 AA.
 AC P82660;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of RMRFamide-related
 RT peptides (FaRPs) from free-living nematode, Panagrellus redivivus."
 RL Submitted (JUL-2000) to Swiss-Prot.
 CC -!- FUNCTION: Myoactive.
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 25.9%; Score 21; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PFPFV 15
 | |||

RESULT 6

YPE2_LACLC

ID YPE2_LACLC STANDARD; PRT; 13 AA.
AC P42021;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PEPT 5' region (ORF2) (Fragment).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245610; PubMed=8188586;
RA Mierau I., Haandrikman A.J., Velterop O., Tan P.S.T., Leenhouts K.L.,
RA Konings W.N., Venema G., Kok J.;
RT "Tripeptidase gene (pepT) of Lactococcus lactis: molecular cloning
RT and nucleotide sequencing of pepT and construction of a chromosomal
RT deletion mutant.";
RL J. Bacteriol. 176:2854-2861(1994).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L27596; AAA20625.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;

Query Match 25.9%; Score 21; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEPF 12

:|||

Db 4 IEPF 7

RESULT 7

UC25_MAIZE

ID UC25_MAIZE STANDARD; PRT; 15 AA.
AC P80631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.9, its MW is: 31.6 kDa.
 DR Maize-2DPAGE; P80631; COLEOPTILE.
 DR MaizeDB; 123957; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1580 MW; 83C54CF0CE1614D0 CRC64;

Query Match 25.9%; Score 21; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PVEPF 12
 ||||
 Db 10 PVEAF 14

RESULT 8

UC30_MAIZE

ID UC30_MAIZE STANDARD; PRT; 15 AA.
 AC P80636;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 662)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.9, its MW is: 32.3 kDa.
 DR Maize-2DPAGE; P80636; COLEOPTILE.
 DR MaizeDB; 123961; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1545 MW; 3485190F4EF38018 CRC64;

Query Match 25.9%; Score 21; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEPF 12
|:| |
Db 5 PLLPAITF 12

RESULT 9

A45K_MYCBO

ID A45K_MYCBO STANDARD; PRT; 17 AA.
AC P80069;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 45/47 kDa antigen (Fragment).
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;
RX MEDLINE=93138802; PubMed=8423100;
RA Romain F., Laqueyrie A., Militzer P., Pescher P., Chavarot P.,
RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;
RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen
RT complex, an immunodominant target for antibody response after
RT immunization with living bacteria.";
RL Infect. Immun. 61:742-750(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: TO M.LEPRAE NL43, AND M.TUBERCULOSIS MPT32.
DR PIR; A49237; A49237.
KW Antigen.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 25.9%; Score 21; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEP 11
| || |
Db 4 PAPPVPP 10

RESULT 10

ALL3_CARMA

ID ALL3_CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -!- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 7;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EPFPF 14
 ||: |
 Db 1 EPYAF 5

RESULT 11

ECDC_LYMDI

ID ECDC_LYMDI STANDARD; PRT; 14 AA.
 AC P80940;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Testis ecdysiotropin peptide C (TE).
 OS *Lymantria dispar* (Gypsy moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Lymantriidae; *Lymantria*.
 OX NCBI_TaxID=13123;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=97387807; PubMed=9243792;
 RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
 RA Bell R.A.;
 RT "Naturally occurring analogs of *Lymantria testis* ecdysiotropin, a
 RT gonadotropin isolated from brains of *Lymantria dispar* pupae.";
 RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
 CC -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of
 CC larvae and pupae.
 SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match 24.7%; Score 20; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PFPF 14
| |
Db 9 PLPF 12

RESULT 12

SODM_STRGR

ID SODM_STRGR STANDARD; PRT; 15 AA.
AC P80733;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).
GN SOD2.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE.
RC STRAIN=KCTC 9006;
RX MEDLINE=97056064; PubMed=8900409;
RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
RA Kang S.-O.;
RT "Unique isozymes of superoxide dismutase in Streptomyces griseus."
RL Arch. Biochem. Biophys. 334:341-348(1996).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron or zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Tetramer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Metal-binding; Iron; Zinc.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 15;
Best Local Similarity 37.5%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LPVEPFPF 14
| | | : :
Db 5 LPEPPYDY 12

RESULT 13

LPK1_LOCFI

ID LPK1_LOCFI STANDARD; PRT; 16 AA.
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 1 (LOM-PK-1).

OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=91224474; PubMed=2026322;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
 RT myotropic peptide of Locusta migratoria.";
 RL Gen. Comp. Endocrinol. 81:97-104(1991).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR PIR; A49761; A49761.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 16 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 16;
 Best Local Similarity 60.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PVEPF 12
 | :||
 Db 8 PQQPF 12

RESULT 14

RT02_BOVIN

ID RT02_BOVIN STANDARD; PRT; 10 AA.
 AC P82923;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).
 GN MRPS2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=21276436; PubMed=11279123;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome:
 RT identification of the full complement of ribosomal proteins present.";
 RL J. Biol. Chem. 276:19363-19374(2001).
 CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.

CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1246 MW; 6A7A6679C04B476B CRC64;

Query Match 23.5%; Score 19; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFPF 14
 :||: |
 Db 2 MEPYIF 7

RESULT 15

CSI5_BACSU

ID CSI5_BACSU STANDARD; PRT; 11 AA.
 AC P81095;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=168 / JH642;
 RA Graumann P.L., Schmid R., Marahiel M.A.;
 RL Submitted (OCT-1997) to Swiss-Prot.
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=168 / JH642;
 RX MEDLINE=96345629; PubMed=8755892;
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
 RT "Cold shock stress-induced proteins in Bacillus subtilis."
 RL J. Bacteriol. 178:4611-4619(1996).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: In response to low temperature.
 CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 11;
 Best Local Similarity 50.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LPVEPF 12
 :|:|
 Db 4 IKVKPF 9

RESULT 16

TY13_PHYRO

ID TY13_PHYRO STANDARD; PRT; 13 AA.
 AC P04096;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tryptophyllin-13.
 OS Phyllomedusa rohdei (Rohde's leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.
 OX NCBI_TaxID=8394;
 RN [1]
 RP SEQUENCE.
 RA Montecucchi P.C., Gozzini L., Erspamer V.;
 RT "Primary structure determination of a tryptophan-containing
 RT tridecapeptide from Phyllomedusa rohdei.";
 RL Int. J. Pept. Protein Res. 27:175-182(1986).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; A05174; A05174.
 KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 13;
 Best Local Similarity 36.4%; Pred. No. 2.6e+03;
 Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 EMPVLPVEFPF 13
 | | | :|
 Db 2 EKPYPPIYP 12

RESULT 17

UC08_MAIZE

ID UC08_MAIZE STANDARD; PRT; 15 AA.
 AC P80614;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown

CC protein is: 6.4, its MW is: 38.8 kDa.
 CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family.
 DR Maize-2DPAGE; P80614; COLEOPTILE.
 DR MaizeDB; 123934; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4DDF8D CRC64;

 Query Match 23.5%; Score 19; DB 1; Length 15;
 Best Local Similarity 75.0%; Pred. No. 3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 PVLP 8
 ||:|
 Db 9 PVVP 12

RESULT 18

GLN2_PINPS

ID GLN2_PINPS STANDARD; PRT; 15 AA.
 AC P81107;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Probable glutamine synthetase leaf isozyme (EC 6.3.1.2) (Glutamate--
 DE ammonia ligase) (S2205/S2287) (N47/N48) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RA Plomion C., Costa P., Bahrman N., Frigerio J.-M.;
 RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
 RT dominant and codominant protein markers assayed on diploid tissue, in
 RT a haploid-based genetic map."
 RL Silvae Genet. 46:161-165(1997).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins."
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- FUNCTION: The light-modulated chloroplast enzyme, encoded by a
 CC nuclear gene and expressed primarily in leaves, is responsible for
 CC the reassimilation of the ammonia generated by photorespiration
 CC (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +
 CC L-glutamine.
 CC -!- SUBUNIT: Homooctamer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:

CC 5.7, its MW is: 42 kDa.
 CC -!- SIMILARITY: Belongs to the glutamine synthetase family.
 DR InterPro; IPR008147; Gln_synt_beta.
 DR InterPro; IPR008146; Gln_synt_C.
 DR PROSITE; PS00180; GLNA_1; PARTIAL.
 DR PROSITE; PS00181; GLNA_ATP; PARTIAL.
 KW Ligase; Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1614 MW; 24A2420BEFD60D27 CRC64;

Query Match 22.8%; Score 18.5; DB 1; Length 15;
 Best Local Similarity 35.7%; Pred. No. 3.6e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 DLEMPV-LPVEFPF 13
 |: |: || :|
 Db 1 DVNWPLGWPVGGYP 14

RESULT 19

UC29_MAIZE

ID UC29_MAIZE STANDARD; PRT; 15 AA.
 AC P80635;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.9, its MW is: 37.6 kDa.
 DR Maize-2DPAGE; P80635; COLEOPTILE.
 DR MaizeDB; 123960; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

Query Match 22.8%; Score 18.5; DB 1; Length 15;
 Best Local Similarity 62.5%; Pred. No. 3.6e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 8 PVEFPFV 15
 || || |
 Db 4 PV-PIPLV 10

RESULT 20

UPA3_HUMAN

ID UPA3_HUMAN STANDARD; PRT; 9 AA.
 AC P30089;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing."
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.6, its MW is: 46 kDa.
 DR SWISS-2DPAGE; P30089; HUMAN.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 9;
 Best Local Similarity 37.5%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PVLPEPF 12
 | : | |
 Db 2 PLFPXTDF 9

RESULT 21

EFG_CLOPA

ID EFG_CLOPA STANDARD; PRT; 11 AA.
 AC P81350;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor G (EF-G) (CP 5) (Fragment).
 GN FUSA.
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;

RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFATOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PVEPF 12
|:| |
Db 3 PLEKF 7

RESULT 22

FIBB_RABIT

ID FIBB_RABIT STANDARD; PRT; 13 AA.
AC P14478;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR InterPro; IPR002181; Fibrinogen_C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.
FT MOD_RES 4 4 SULFATION.
FT NON_TER 13 13

SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;

Query Match 22.2%; Score 18; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLEMPVLP 8
| : |||
Db 3 DYDDEVLP 10

RESULT 23

PEDI_HYDAT

ID PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris."
RL Development 122:1941-1948(1996).
CC -!- FUNCTION: Morphogenetically active peptide. Active in foot
CC development.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 22.2%; Score 18; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLEMPVLP 8
:| |||
Db 2 ELRPEVLP 9

RESULT 24

SODM_CANFA

ID SODM_CANFA STANDARD; PRT; 13 AA.
AC P54712;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
GN SOD2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.
 DR HSC-2DPAGE; P54712; DOG.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1476 MW; 9C9651DE8BE0672A CRC64;

Query Match 22.2%; Score 18; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 3.7e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MPVLPVE 10
 :| || :
 Db 4 LPDLPYD 10

RESULT 25

TEME_RANTE

ID TEME_RANTE STANDARD; PRT; 13 AA.
 AC P56920;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Temporin E.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 RT temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive
 CC bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the brevinin family.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
 |||:
 Db 1 VLPI 4

RESULT 26

ATP6_SPIOL

ID ATP6_SPIOL STANDARD; PRT; 14 AA.
 AC P80086;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ATP synthase A chain (EC 3.6.3.14) (Protein 6) (Fragment).
 GN ATP6.
 OS Spinacia oleracea (Spinach).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Medania; TISSUE=Leaf mesophyll;
 RX MEDLINE=92209531; PubMed=1313368;
 RA Hamasur B., Glaser E.;
 RT "Plant mitochondrial F0F1 ATP synthase. Identification of the
 RT individual subunits and properties of the purified spinach leaf
 RT mitochondrial ATP synthase."
 RL Eur. J. Biochem. 205:409-416(1992).
 CC -!- FUNCTION: Key component of the proton channel; it may play a
 CC direct role in the translocation of protons across the membrane.
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
 CC core - and CF(0) - the membrane proton channel. CF(1) has five
 CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
 CC has three main subunits: a, b and c.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the ATPase A chain family.
 DR PIR; S21247; S21247.
 DR InterPro; IPR000568; ATPsynt_Asub.
 DR PROSITE; PS00449; ATPASE_A; PARTIAL.
 KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1619 MW; 9F1D60181FC1FF45 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 14;

Best Local Similarity 60.0%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 PVEPF 12
|:| |
Db 2 PLEQF 6

RESULT 27

UC15_MAIZE

ID UC15_MAIZE STANDARD; PRT; 14 AA.
AC P80621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.8, its MW is: 35.7 kDa.
DR Maize-2DPAGE; P80621; COLEOPTILE.
DR MaizeDB; 123947; -.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 14;
Best Local Similarity 42.9%; Pred. No. 4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MPVLPVE 10
:|: |
Db 5 LPVVAAE 11

RESULT 28

AF1S_MALPA

ID AF1S_MALPA STANDARD; PRT; 16 AA.
AC P83140;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 1 small subunit (CW-1) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
 OX NCBI_TaxID=145753;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Seed;
 RX MEDLINE=20568734; PubMed=11118343;
 RA Wang X., Bunkers G.J.;
 RT "Potent heterologous antifungal proteins from cheeseweed (*Malva*
 RT *parviflora*).";
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
 CC -!- FUNCTION: Possesses antifungal activity against *F.graminearum*.
 CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
 CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
 CC concentration.
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.
 KW Fungicide; Antibiotic.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1888 MW; 2893A1C66F5D3F57 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 16;
 Best Local Similarity 60.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 PVEPF 12
 | ||
 Db 1 PAGPF 5

RESULT 29

GPX4_PINPS

ID GPX4_PINPS STANDARD; PRT; 17 AA.
 AC P81087;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Glutathione peroxidase homolog (EC 1.11.1.9) (Water stress responsive
 DE proteins 8 and 9) (Fragment).
 OS *Pinus pinaster* (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; *Pinus*.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=98418576; PubMed=9747804;
 RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
 RT "Water-deficit-responsive proteins in maritime pine.";
 RL Plant Mol. Biol. 38:587-596(1998).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";

RL Electrophoresis 20:1098-1108(1999).
 CC -!- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 CC glutathione + 2 H(2)O.
 CC -!- INDUCTION: By water stress.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:
 CC 5.6 to 6.7, its MW is: 20 to 23 kDa.
 CC -!- SIMILARITY: Belongs to the glutathione peroxidase family.
 DR InterPro; IPR000889; Glut_peroxidase.
 DR Pfam; PF00255; GSHPx; 1.
 DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; PARTIAL.
 DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Peroxidase; Oxidoreductase.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1943 MW; 4D245E9B657868C1 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 17;
 Best Local Similarity 36.4%; Pred. No. 4.9e+03;
 Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LEMPVLPVEPF 12
 ||: | |
 Db 6 LEILAFPCNQF 16

RESULT 30

HEMH_THETS

ID HEMH_THETS STANDARD; PRT; 18 AA.
 AC P80155;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ovohemerythrin (YP14) (Fragment).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 OX NCBI_TaxID=13286;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Oocyte;
 RX MEDLINE=93049299; PubMed=1425663;
 RA Baert J.-L., Britel M., Sautiere P., Malecha J.;
 RT "Ovohemerythrin, a major 14-kDa yolk protein distinct from
 RT vitellogenin in leech."
 RL Eur. J. Biochem. 209:563-569(1992).
 CC -!- FUNCTION: Major yolk protein. This iron protein may play a role
 CC in the detoxification of free iron after a blood meal.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the hemerythrin family.
 DR PIR; S29264; S29264.
 DR HSSP; P02247; 2MHR.
 DR InterPro; IPR002063; Hemerythrin.
 DR Pfam; PF01814; Hemerythrin; 1.
 DR PROSITE; PS00550; HEMERYTHRINS; PARTIAL.
 KW Oxygen transport; Metal-binding; Iron; Yolk.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2368 MW; 33397EEE587C81F1 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EPF 12
|||
Db 5 EPF 7

RESULT 31

ALL4_CARMA

ID ALL4_CARMA STANDARD; PRT; 7 AA.
AC P81807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 4.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA; 782 MW; 672879CDCB476AC0 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EPFPF 14
:|: |
Db 1 DPYAF 5

RESULT 32

CARP_MYTED

ID CARP_MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
OC Mytiloidea; Mytilidae; Mytilus.

OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88052022; PubMed=3676797;
 RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
 RA Muneoka Y.;
 RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia."
 RL Brain Res. 422:374-376(1987).
 CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)
 CC and inhibitory (relaxation) effects on the anterior byssus
 CC retractor muscle.
 DR PIR; A29342; ECMUCR.
 KW Hormone; Amidation.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPVL 7
 ||:
 Db 2 MPML 5

RESULT 33

AL10_CARMA

ID AL10_CARMA STANDARD; PRT; 9 AA.
 AC P81813;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 10.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas."
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -!- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 963 MW; 372D79CDCB4776C7 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EPFPF 14
:|: |
Db 3 QPYAF 7

RESULT 34

LMT3_LOCFI

ID LMT3_LOCFI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family."
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: Potent mediator of visceral muscle contractile activity
CC (myotropic activity).
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFV 15
|||
Db 4 PFV 6

RESULT 35

ANG1_BOTJA

ID ANG1_BOTJA STANDARD; PRT; 10 AA.
AC Q10581;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide I (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca.";
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -!- SIMILARITY: Belongs to the serpin family.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPF 12
 | ||
 Db 5 VHPF 8

RESULT 36

ANGT_BOVIN

ID ANGT_BOVIN STANDARD; PRT; 10 AA.
 AC P01017;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 DE (Fragment).
 GN AGT OR SERPINA8.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RA Elliott D.F., Peart W.S.;
 RT "The amino acid sequence in a hypertensin.";
 RL Biochem. J. 65:246-254(1957).
 CC -!- FUNCTION: In response to lowered blood pressure, the enzyme renin
 CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
 CC converting enzyme) then removes a dipeptide to yield the
 CC physiologically active peptide angiotensin II, the most potent
 CC pressor substance known, which helps regulate volume and mineral
 CC balance of body fluids.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -!- SIMILARITY: Belongs to the serpin family.
 DR PIR; A90345; A90345.

DR PDB; 3ER5; 15-JUL-92.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPF 12
 | |
 Db 5 VHPF 8

RESULT 37

ANGT_CHICK

ID ANGT_CHICK STANDARD; PRT; 10 AA.
 AC P01018;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 DE (Fragment).
 GN AGT OR SERPINA8.
 OS Gallus gallus (Chicken), and
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031, 93934;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Chicken;
 RX MEDLINE=74127845; PubMed=4361802;
 RA Nakayama T., Nakajima T., Sokabe H.;
 RT "Comparative studies on angiotensins. 3. Structure of fowl
 RT angiotensin and its identification by DNS-method.";
 RL Chem. Pharm. Bull. 21:2085-2087(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.c.japonica;
 RX MEDLINE=90284684; PubMed=2191893;
 RA Takei Y., Hasegawa Y.;
 RT "Vasopressor and depressor effects of native angiotensins and
 RT inhibition of these effects in the Japanese quail.";
 RL Gen. Comp. Endocrinol. 79:12-22(1990).
 CC -!- FUNCTION: In response to lowered blood pressure, the enzyme renin
 CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
 CC converting enzyme) then removes a dipeptide to yield the
 CC physiologically active peptide angiotensin II, the most potent
 CC pressor substance known, which helps regulate volume and mineral

CC balance of body fluids.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -!- SIMILARITY: Belongs to the serpin family.
 DR PIR; A60624; A60624.
 DR PIR; A90917; A90917.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPF 12
 | | |
 Db 5 VHPF 8

RESULT 38

ANGT_CRIGE

ID ANGT_CRIGE STANDARD; PRT; 11 AA.
 AC P09037;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Crinia-angiotensin II.
 OS Crinia georgiana (Quacking frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Crinia.
 OX NCBI_TaxID=8374;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80024575; PubMed=488254;
 RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endecapeptide from the skin of the Australian
 RT frog Crinia georgiana.";
 RL Experientia 35:1132-1133(1979).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S07207; S07207.
 KW Vasoconstrictor.
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 21.0%; Score 17; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPF 12

Db | ||
 8 VHPF 11

RESULT 39

BPP_AGKHP

ID BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 4.5e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PVLPEP 11
 | | : |
Db 5 PGPPIPP 11

RESULT 40

MP1_MICOC

ID MP1_MICOC STANDARD; PRT; 13 AA.
AC P81532;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE MP1 protein (Fragments).
OS Microplitis ocellatae (Braconid wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
OC Braconidae; Microgastrinae; Microplitis.

OX NCBI_TaxID=99573;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RA Takahashi M., Quicke D.L.J.;
 RL Submitted (OCT-1998) to Swiss-Prot.
 CC -!- TISSUE SPECIFICITY: Salivary glands.
 CC -!- DEVELOPMENTAL STAGE: LARVAL.
 FT NON_CONS 10 11
 SQ SEQUENCE 13 AA; 1595 MW; 0C0786C9DD82777B CRC64;

Query Match 21.0%; Score 17; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 5.4e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFP 13
 |:
 Db 5 PYP 7

RESULT 41

CBPB_PROAT

ID CBPB_PROAT STANDARD; PRT; 15 AA.
 AC P19628;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carboxypeptidase B (EC 3.4.17.2) (Fragment).
 OS Protopterus aethiopicus (Marbled lungfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Dipnoi; Lepidosireniformes; Protopteridae; Protopterus.
 OX NCBI_TaxID=7886;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=73025047; PubMed=5079891;
 RA Reeck G.R., Neurath H.;
 RT "Isolation and characterization of pancreatic procarboxypeptidase B
 RT and carboxypeptidase B of the African lungfish."
 RL Biochemistry 11:3947-3955(1972).
 CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysine(or L-arginine) + H(2)O =
 CC peptide + L-lysine(or L-arginine).
 CC -!- SIMILARITY: Belongs to peptidase family M14.
 DR PIR; A26212; A26212.
 DR MEROPS; M14.003; -.
 DR InterPro; IPR000834; Peptidase_M14.
 DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; PARTIAL.
 DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; PARTIAL.
 KW Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Zymogen.
 FT PROPEP 1 >15 ACTIVATION PEPTIDE.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1749 MW; 124C910D937BED65 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 15;
 Best Local Similarity 75.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 EPFP 13
|||
Db 1 EPTP 4

RESULT 42

SAL1_ONCMY

ID SAL1_ONCMY STANDARD; PRT; 15 AA.
AC P81369;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Salmocidin 1 (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Serum;
RA Henry M.A., Siegert K.J., Davidson I., Dunbar B., Mordue W.,
RA Secombes C.J.;
RT "Isolation and N-terminal sequencing of an antibacterial peptide in
RT rainbow trout, Oncorhynchus mykiss."
RL Submitted (MAY-1998) to Swiss-Prot.
CC -!- FUNCTION: Antibacterial peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma serum.
KW Antibiotic.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1586 MW; 3AF4AD95AFAB26D0 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LPVEP 11
|||
Db 11 LPAXP 15

RESULT 43

UBL1_MONDO

ID UBL1_MONDO STANDARD; PRT; 15 AA.
AC P50103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5)
DE (PGP 9.5) (PGP9.5) (Fragment).
GN UCHL1.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96102916; PubMed=8522974;
 RA Mann D.A., Trowern A.R., Lavender F.L., Whittaker P.A.,
 RA Thompson R.J.;
 RT "Identification of evolutionary conserved regulatory sequences in the
 RT 5' untranscribed region of the neural-specific ubiquitin C-terminal
 RT hydrolase (PGP9.5) gene.";
 RL J. Neurochem. 66:35-46(1996).
 CC -!- FUNCTION: Ubiquitin-protein hydrolase is involved both in the
 CC processing of ubiquitin precursors and of ubiquitinated proteins.
 CC This enzyme is a thiol protease that recognizes and hydrolyzes
 CC a peptide bond at the C-terminal glycine of ubiquitin.
 CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
 CC ubiquitin + a thiol.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to peptidase family C12.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; U32208; AAA89059.1; -.
 DR InterPro; IPR001578; Peptidase_C12.
 DR PROSITE; PS00140; UCH_1; PARTIAL.
 KW Ub1 conjugation pathway; Hydrolase; Thiol protease; Multigene family.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1816 MW; 1B7A3B6E623F6E79 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 15;
 Best Local Similarity 40.0%; Pred. No. 6.3e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 MPVLPVEFPF 13
 | : | : | |
 Db 1 MQLKPMEINP 10

RESULT 44

FOR2_MYRGU

ID FOR2_MYRGU STANDARD; PRT; 16 AA.
 AC P81437;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Formaecin 2.
 OS Myrmecia gulosa (Red bulldog ant).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Formicidae; Myrmeciinae; Myrmeciini; Myrmecia.
 OX NCBI_TaxID=36170;
 RN [1]

RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
 RC TISSUE=Hemolymph;
 RX MEDLINE=98165787; PubMed=9497332;
 RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
 RT "Isolation from an ant *Myrmecia gulosa* of two inducible
 RT O-glycosylated proline-rich antibacterial peptides.";
 RL J. Biol. Chem. 273:6139-6143(1998).
 CC -!- FUNCTION: Antibacterial peptide. Has activity against E.coli but
 CC none against other Gram-negative bacteria and Gram-positive
 CC bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- INDUCTION: By bacterial infection.
 CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
 CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
 FT CARBOHYD 11 11 O-LINKED (GALNAC. . .).
 SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 21.0%; Score 17; DB 1; Length 16;
 Best Local Similarity 66.7%; Pred. No. 6.7e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PFP 13
 | : |
 Db 12 PYP 14

RESULT 45

PSBL_SYNVU

ID PSBL_SYNVU STANDARD; PRT; 17 AA.

AC P12241;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Photosystem II reaction center L protein (PSII 5 kDa protein)

DE (Fragment).

GN PSBL.

OS *Synechococcus vulcanus* (*Thermosynechococcus vulcanus*).

OC Bacteria; Cyanobacteria; Chroococcales; *Thermosynechococcus*.

OX NCBI_TaxID=32053;

RN [1]

RP SEQUENCE.

RA Ikeuchi M., Koike H., Inoue Y.;

RT "Identification of psbI and psbL gene products in cyanobacterial

RT photosystem II reaction center preparation.";

RL FEBS Lett. 251:155-160(1989).

CC -!- FUNCTION: Not known, it is however required for PSII activity.

CC -!- SUBCELLULAR LOCATION: Cellular thylakoid membrane.

CC -!- SIMILARITY: Belongs to the psbL family.

DR PIR; S05033; S05033.

DR HAMAP; MF_01317; -; 1.

DR InterPro; IPR003372; PSII_PsbL.

DR Pfam; PF02419; PsbL; 1.

KW Photosynthesis; Thylakoid; Photosystem II; Reaction center.

FT NON_TER 17 17

SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;

Query Match 21.0%; Score 17; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPFP 13
: || |
Db 1 MEPNP 5

RESULT 46

ALL2_CYPDPO

ID ALL2_CYPDPO STANDARD; PRT; 18 AA.
AC P82153;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 2.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily."
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 18 18 AMIDATION.
SQ SEQUENCE 18 AA; 2169 MW; 8E66679C0CDF175C CRC64;

Query Match 21.0%; Score 17; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 LPVEPF 12
| | | |
Db 11 LPVYNF 16

RESULT 47

ANG2_BOTJA

ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.

OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca.";
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -!- SIMILARITY: Belongs to the serpin family.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 19.8%; Score 16; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 VEPF 12
 : ||
 Db 5 IHPF 8

RESULT 48

UPA7_HUMAN

ID UPA7_HUMAN STANDARD; PRT; 9 AA.
 AC P30093;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.05, its MW is: 37 kDa.
 DR SWISS-2DPAGE; P30093; HUMAN.
 FT NON_TER 1 1
 FT UNSURE 5 5
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

Query Match 19.8%; Score 16; DB 1; Length 9;
 Best Local Similarity 28.6%; Pred. No. 1.4e+05;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VLPVEPF 12
 ::| |:
 Db 2 LVPEXPY 8

RESULT 49

TMOF_AEDAE

ID TMOF_AEDAE STANDARD; PRT; 10 AA.
 AC P19425;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
 OX NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Vero beach; TISSUE=Ovary;
 RX MEDLINE=90367888; PubMed=2394318;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mosquito oostatic factor: a novel decapeptide modulating
 RT trypsin-like enzyme biosynthesis in the midgut.";
 RL FASEB J. 4:3015-3020(1990).
 RN [2]
 RP SEQUENCE.
 RC STRAIN=Vero beach; TISSUE=Ovary;
 RX MEDLINE=93357794; PubMed=8353526;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mass spectrometry and characterization of Aedes aegypti trypsin
 RT modulating oostatic factor (TMOF) and its analogs.";
 RL Insect Biochem. Mol. Biol. 23:703-712(1993).
 CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
 CC in the midgut which indirectly reduces the vitellogenin
 CC concentration in the hemolymph resulting in inhibition of oocyte
 CC development.
 CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
 CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at
 CC 36 hrs and stops at 56 hrs.
 DR PIR; A36454; A36454.
 KW Hormone.
 FT DOMAIN 3 10 POLY-PRO.
 FT VARIANT 1 2 YD -> DY (IN TMFO(B)).
 SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;

Query Match 19.8%; Score 16; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 PVEFPF 13
 | | |
 Db 3 PAPPPP 8

RESULT 50

UHA3_HUMAN

ID UHA3_HUMAN STANDARD; PRT; 10 AA.
 AC P40930;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 RT 1994."
 RL Electrophoresis 15:1459-1465(1994).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.8, its MW is: 47.3 kDa.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;

Query Match 19.8%; Score 16; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEP 11
 |||
 Db 2 VEP 4

Search completed: July 4, 2004, 04:41:29
 Job time : 6.14925 secs